

GenCore version 5.1.4.p5.4578  
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## OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 07:42:38 ; Search time 1893 Seconds  
(without alignments)  
3766.607 Million cell updates/sec

Title: US-09-744-502-20

Perfect score: 245  
Sequence: 1 ttagagggaataaaagtc.....tgaacgcatcataaact 245

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	100.0	675	8 RSP242875	AJ242875 Rhizocton
2	238.6	97.4	652	8 RSP242879	AJ242879 Rhizocton
3	235.4	96.1	661	8 RSP242880	AJ242880 Rhizocton
4	234.6	95.8	668	8 RSP242877	AJ242877 Rhizocton
5	231.6	94.5	654	8 RSP242878	AJ242878 Rhizocton
6	231.2	94.4	657	8 RSP242876	AJ242876 Rhizocton
7	229.8	93.8	660	8 RSP242885	AJ242885 Rhizocton
8	225.6	92.1	661	8 RSP242886	AJ242886 Rhizocton
9	216.4	88.3	665	8 RSP242881	AJ242881 Rhizocton
10	174	71.0	659	8 RSP242897	AJ242897 Rhizocton
11	166.2	67.8	661	8 RSP242898	AJ242898 Rhizocton
12	166.2	67.8	661	8 RSP242899	AJ242899 Rhizocton
13	144	58.8	661	8 RSP242892	AJ242892 Rhizocton
14	142.6	58.2	664	8 RSP242902	AJ242902 Rhizocton
15	140.8	57.5	661	8 RSP242893	AJ242893 Rhizocton
16	137.2	56.0	626	8 AF461605	AF461605 Unculture
17	135.6	55.3	647	8 RSP242883	AJ242883 Rhizocton
18	133.6	54.5	698	8 RSP242903	AJ242903 Rhizocton
19	122	49.8	635	8 RSP242884	AJ242884 Rhizocton
20	117.2	47.8	655	8 RSP242894	AJ242894 Rhizocton
21	117.2	47.8	656	8 RSP242895	AJ242895 Rhizocton
22	114.8	46.9	641	8 RSP242882	AJ242882 Rhizocton
23	112	45.7	669	8 RSP242887	AJ242887 Rhizocton
24	111.6	45.6	1491	8 AF354094	AF354094 Ceratobas
25	108.2	44.2	649	8 RSP242890	AJ242890 Rhizocton
26	108.2	44.2	656	8 RSP242896	AJ242896 Rhizocton
27	106.6	43.5	649	8 RSP242891	AJ242891 Rhizocton
28	106.6	43.5	854	8 AF200518	AF200518 Rhizocton
29	106.6	43.5	854	8 AF200519	AF200519 Rhizocton
30	104.8	42.8	701	8 RSP242900	AJ242900 Ceratobas
31	104.6	42.7	589	8 CC0301900	AJ301900 Ceratobas
32	103.2	42.1	605	8 FU419931	AJ419931 Rhizocton
33	100.6	41.1	591	8 RSU19963	U19963 Rhizoctonia
34	98.2	40.1	692	8 RSP242901	AJ242901 Rhizocton
35	97.6	39.8	1477	8 AF354093	AF354093 Ceratobas
36	96.4	39.3	590	8 CC0302006	AJ302006 Ceratobas
37	96	39.2	860	8 AF200516	AF200516 Rhizocton
38	96	39.2	860	8 AF200517	AF200517 Rhizocton
39	95.6	39.0	590	8 RSU19962	U19962 Rhizoctonia
40	94.4	38.5	591	8 CC0301899	AJ301899 Ceratobas
41	94.4	38.5	594	8 CC0301903	AJ301903 Ceratobas
42	92.8	37.9	576	8 CC0301902	AJ301902 Ceratobas
43	87.4	35.7	578	8 AF502772	AF502772 Leaf lilt
44	86.4	35.3	850	8 AF200520	AF200520 Rhizocton
45	86.2	35.2	585	8 CC0301901	AJ301901 Ceratobas

## ALIGNMENTS

RESULT 1  
RSP242875 675 bp DNA linear PLN 15-JAN-2002  
LOCUS Rhizoctonia sp. Eab-F1 5.8S rRNA gene and ITS1 and 2, strain  
DEFINITION Eab-F1.  
ACCESSION AJ242875  
VERSION AJ242875.1 GI:18181597  
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;  
internal transcribed spacer 2; ITS1; ITS2.  
SOURCE Rhizoctonia sp. Eab-F1.  
ORGANISM Rhizoctonia sp. Eab-F1  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;  
Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiaceae;  
Ceratobasidiaceae; Ceratobasidiaceae; Rhizoctonia.

## REFERENCE

1

FEATURES	source
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 675)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biología Microbiana, Centro Nacional de Biotecnología, Campus Cantoblanco, Universidad Autónoma de Madrid, Madrid 28049, SPAIN
LOCATION/Qualifiers	
1. 675	/organism="Rhizoctonia sp. Eab-F1"
/strain="Eab-F1"	
/db_xref="taxon:193679"	
/country="Spain"	
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misc-feature	/note="internal transcribed spacer 1, (ITS1)"
246. 400	
gene	/gene="5.8S rRNA"
246. 400	
rRNA	/gene="5.8S rRNA"
/product="5.8S ribosomal RNA"	
401. >675	
misc-feature	/note="internal transcribed spacer 2, (ITS2)"
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Query Match	100.0%; Score 245; DB 8; Length 675;
Best Local Similarity	100.0%; Pred. NO. 8.5e-57;
Matches 245; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
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1	TTAGAGGGGAAATAAAGTCTGTACAGAGTTTCCTAGCTGACCTGCGAAGATCATT 60
61	ATTGATGATATATACAGTTGGTTGCTGCTGCTCCTCGGAGCATGTGCACGCTTCTC 120
61	ATTGATGATATATACAGTTGGTTGCTGCTGCTCCTCGGAGCATGTGCACGCTTCTC 120
121	TTTCATCCACACACACGCTGTGACCTGTGAGACGAGGACCGCTAAAAAAGTCTCCGCT 180
121	TTTCATCCACACACACGCTGTGACCTGTGAGACGAGGACCGCTAAAAAAGTCTCCGCT 180
181	ATTAAACCAACAACCCCATTTGTTAAATTTGAATGTAATTTGATGTACCATCATTA 240
181	ATTAAACCAACAACCCCATTTGTTAAATTTGAATGTAATTTGATGTACCATCATTA 240
241	AAACT 245
241	AAACT 245
RESULT 2	
LOCUS	RSP242879 652 bp DNA linear PLN 15-JAN-2002
DEFINITION	Rhizoctonia sp. Eab-F6 5.8S rRNA gene and ITS1 and 2, strain Eab-F6.
ACCESSION	AJ242879
VERSION	AJ242879.1 GI:18181601
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-F6.
ORGANISM	Rhizoctonia sp. Eab-F6.
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
AUTHORS	Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
TITLE	Ceratobasidiaceae; Ceratobasidiaceae; Rhizoctonia.
1	Salazar O., Munoz R., Lopez-Corcoles H. and Rubio V.
1	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 652)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers
source	1..652
	/organism="Rhizoctonia sp. Eab-F6"
	/strain="Eab-F6"
	/db_xref="taxon:183683"
	/country="Spain"
misc-feature	<1..246
gene	/note="Internal transcribed spacer 1, (ITS1)"
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rrna	/gene="5.8S rRNA"
	247..401
	/gene="5.8S rRNA"
misc-feature	/product="5.8S ribosomal RNA"
	402..>652
	/note="Internal transcribed spacer 2, (ITS2)"
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Query Match	97.4%; Score 238.6; DB 8; Length 652;
Best Local Similarity	98.4%; Pred. No. 4, 8e-55;
Matches 241; Conservative	0; Mismatches 4; Indels 0; Gaps 0
QY	1 TTAAGGGGAATATAAAAGTCGTACACAGGTTTCCGTAGTGTAACCTGCGGAGGATCATTT 60
Db	2 TTAGAGGGGAATATAAAAGTCGTACACAGGTTTCCGTAGTGTAACCTGCGGAGGATCATTT 61
QY	61 ATTGATGATGAATTTAAGTGTGTTTCGCGGCGCTCCCGGAGCATGTGCACGCTTCTC 120
Db	62 ATTGATGATGAATTTAAGTGTGTTTCGCGCTCCCGGAGCATGTGCACACTTCTC 121
QY	121 TTTCATCCACACACACCTGTGCACCTTGTGAGACGAGACCCGTAATAAAAGTTCGCTCT 180
Db	122 TTTCATCCACACACACCTGTGCACCTTGTGAGACGAGACCCGTAATAAAAGTTCGCTCT 181
QY	181 ATTAACCAACACAAACCCATGTTAATTGAATGAATGAATGAATGAATGAATGAATGAATGAAT 240
Db	182 ATTAACCAACACAAACCCATGTTAATTGAATGAATGAATGAATGAATGAATGAATGAATGAAT 241
QY	241 AAAT 245
Db	242 GAAT 246
RESULT 3	
LOCUS	RSP242880 661 bp DNA linear PLN 15-JAN-2001
DEFINITION	Rhizoctonia sp. Eab-F7 5.8S rRNA gene and ITS1 and 2, strain Eab-F7.
ACCESSION	AJ242880
VERSION	AJ242880.1 GI:18181602
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer 1; Internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-F7.
ORGANISM	Rhizoctonia sp. Eab-F7
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Ceratobasidiales; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
REFERENCE	1 Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
AUTHORS	Molecular characterization and pathogenicity of a new group of
TITLE	isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.)
JOURNAL	isolated in Spain
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 661)
TITLE	Julian M.C.
	Direct Submission

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 652)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers
source	1..652
	/organism="Rhizoctonia sp. Eab-F6"
	/strain="Eab-F6"
	/db_xref="taxon:183683"
	/country="Spain"
misc-feature	<1..246
gene	/note="Internal transcribed spacer 1, (ITS1)"
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	/gene="5.8S rRNA"
misc-feature	/product="5.8S ribosomal RNA"
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BASE COUNT	190 a 126 c 138 g 198 t
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Query Match	97.4%; Score 238.6; DB 8; Length 652;
Best Local Similarity	98.4%; Pred. No. 4, 8e-55;
Matches 241; Conservative	0; Mismatches 4; Indels 0; Gaps 0
QY	1 TTAAGGGGAATATAAAAGTCGTACACAGGTTTCCGTAGTGTAACCTGCGGAGGATCATTT 60
Db	2 TTAGAGGGGAATATAAAAGTCGTACACAGGTTTCCGTAGTGTAACCTGCGGAGGATCATTT 61
QY	61 ATTGATGATGAATTTAAGTGTGTTTCGCGGCGCTCCCGGAGCATGTGCACGCTTCTC 120
Db	62 ATTGATGATGAATTTAAGTGTGTTTCGCGCTCCCGGAGCATGTGCACACTTCTC 121
QY	121 TTTCATCCACACACACCTGTGCACCTTGTGAGACGAGACCCGTAATAAAAGTTCGCTCT 180
Db	122 TTTCATCCACACACACCTGTGCACCTTGTGAGACGAGACCCGTAATAAAAGTTCGCTCT 181
QY	181 ATTAACCAACACAAACCCATGTTAATTGAATGAATGAATGAATGAATGAATGAATGAATGAAT 240
Db	182 ATTAACCAACACAAACCCATGTTAATTGAATGAATGAATGAATGAATGAATGAATGAATGAAT 241
QY	241 AAAT 245
Db	242 GAAT 246
RESULT 3	
LOCUS	RSP242880 661 bp DNA linear PLN 15-JAN-2001
DEFINITION	Rhizoctonia sp. Eab-F7 5.8S rRNA gene and ITS1 and 2, strain Eab-F7.
ACCESSION	AJ242880
VERSION	AJ242880.1 GI:18181602
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer 1; Internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-F7.
ORGANISM	Rhizoctonia sp. Eab-F7
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Ceratobasidiales; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
REFERENCE	1 Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
AUTHORS	Molecular characterization and pathogenicity of a new group of
TITLE	isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.)
JOURNAL	isolated in Spain
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 661)
TITLE	Julian M.C.
	Direct Submission

## JOURNAL

Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnología Microbiana, Centro Nacional de Biotecnología, Campus Cantoblanco, Universidad Autónoma de Madrid, Madrid 28049, SPAIN

## FEATURES

## source

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/organism="Rhizoctonia sp. Eab-F7"

/strain="Eab-F7"

/db\_xref="taxon:183684"

/country="Spain"

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/note="internal transcribed spacer 1, (ITS1)"

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## misc-feature

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## QY

1 TTAGAGGGGAAATAAAAGTCGTAACAAGTTTCCTGAGTGAACCTGCGAGAGATCAT 60

## Db

8 TTTTAAAGAGAAAGTAAAGTCTAACAAGTTTCCTGAGTGAACCTGCGAGAGATCAT 67

## QY

61 ATTGAATGATATATAGATGTTGTTGCTGCTGCTCCGGAGACATGTGACGCTTCTC 120

## Db

68 ATTGAATGATATATAGATGTTGTTGCTGCTGCTCCGGAGACATGTGACGCTTCTC 127

## QY

121 TTTCATCCACACACACCTGTCGACCTGTGAGAGGAGACCGTAAAGTTTCCGCTC 180

## Db

128 TTTCATCCACACACACCTGTCGACCTGTGAGAGGAGACCGTAAAGTTTCCGCTC 187

## QY

181 ATTAAACCAACAACCCCATTTGATTTAATGAATGAATGAATGAATGAATGAATGA 240

## Db

188 ATTAAACCAACAACCCCATTTGATTTAATGAATGAATGAATGAATGAATGAATGA 247

## QY

241 AACT 245

## Db

248 GAAC 252

## RESULT 4

## RSP242877

## LOCUS

## DEFINITION

## Eab-F3.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## AUTHORS

## TITLE

## JOURNAL

## AUTHORS

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## TITLE

## JOURNAL

## AUTHORS

## TITLE

## source

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/organism="Rhizoctonia sp. Eab-F3"

/strain="Eab-F3"

/db\_xref="taxon:183681"

/country="Spain"

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ORIGIN			196 t
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Best Local Similarity	98.3%;	Pred. No. 4e-53;	
Matches 234; Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;
Oy	8	GGAATAAAAAGCGCTAACAAAGTTCCGTAGGTGAACCTCGCGAAGAGATCATATTGAAT	67
Db	1	GGAAGTAAAAAGCGTAACAAAGGTTCCGTAGGTGAACCTCGCGAAGAGATCATATTGAAT	60
Oy	68	GAATATAGAGTTGGTTGTCGCTGCGCTCCGCGAGAGCATGTCCACGCTTCTCTTCATC	127
Db	61	GAATATAGAGTTGGTTGTCGCTGCGCTCCGCGAGAGCATGTCCACGCTTCTCTTCATC	120
Oy	128	CACACACACCTGTGCAGCTTGTGAGACGAGACCGCTAAAAAGTCTTCGCTATTAAAC	187
Db	121	CACACACACCTGTGCAGCTTGTGAGACGAGACCGCTAAAAAGTCTTCGCTATTAAAC	180
Oy	188	CACACAAACCCATGTATTTTAAATTGAATGTAATGTATTAACCATCATTAACACT	245
Db	181	CACACAAACCCATGTATTTTAAATTGAATGTAATGTATTAACCATCATTAAGAACT	238

FEATURES	source
LOCUS	RSP242876 657 bp DNA linear PLN 15-JAN-2002
DEFINITION	Rhizoctonia sp. Eab-F2 5.8S rRNA gene and ITS1 and 2, strain Eab-F2.
ACCESSION	AJ242876
VERSION	AJ242876.1 GI:18181598
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-F2.
ORGANISM	Rhizoctonia sp. Eab-F2
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
AUTHORS	1 Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
TITLE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 657)
AUTHORS	Julian, M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
FEATURES	location/Qualifiers
source	1..657
	/organism="Rhizoctonia sp. Eab-F2"
	/strain="Eab-F2"
	/db_xref="taxon:183680"
	/country="Spain"
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misc_feature	/note="internal transcribed spacer 1, (ITS1)"
gene	243..397
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		/note="internal transcribed spacer 2, (ITS2)"	
BASE COUNT	188 a	131 c	143 g
ORIGIN			195 t
Query Match		94.4%; Score 231.2; DB 8;	Length 657;
Best Local Similarity		98.7%; Pred. No. 5.2e-53;	
Matches	233; Conservative	0; Mismatches	3; Indels 0; Gaps 0;
QY	5	AGGGGATTAANAAGTCGTACCAAGTTCCTCCGTAGTGAACTCGCGGANGAGATCATTTATTG	64
Dd	1	AGAGGAAGTAAAGAAGCTGTACCAAGGTTCCGTAGTGTGAACGCAGGAGATCATTTATTG	60
QY	65	AATGAATTTAAGAGTTGGTTGCCGTGCGGCTCCTCCGCGGAGCANTGACAGCTTTTCCTTC	124
Dd	61	AATGAATTTAAGAGTTGGTTGCCGTGCGGCTCCTCCGCGGAGCANTGACAGCTTTTCCTTC	120
OY	125	ATCCACACACACTGTGTGACTTGTGAGACGGAGACCGTAAAAAGCTCCCGTATTATA	184
Dd	121	ATCCACACACACTGTGTGACTTGTGAGACGGAGACCGTAAAAAGCTTCGCTATATA	180
QY	185	AACGACACAACCCTATGTATTTTAAATTGAAATGAAATGATGTAACCATCATTA	240
Dd	181	AACGACACAACCCTATGTATTTTAAATTGAAATGAAATGATGTAACCATCATTA	236

RESULT	7
RSP242885	660 bp DNA linear PLN_15-JAN-2002
LOCUS	RSP242885
DEFINITION	Rhizoctonia sp. Eab-S5 5.8S rRNA gene and ITS1 and 2, strain Eab-S5.
ACCESSION	AJ242885
VERSION	AJ242885.1 GI:18181607
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-S5
ORGANISM	Rhizoctonia sp. Eab-S5 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
REFERENCE	1 Salazar,O., Munoz,R., Lopez-Corcoles,H. and Rubio,V. Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
AUTHORS	Unpublished
JOURNAL	2 (bases 1 to 660)
REFERENCE	Julian,M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiolana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers
source	1..660 /organism="Rhizoctonia sp. Eab-S5" /strain="Eab-S5" /dn_xref="taxon:183689" /country="Spain" <1..236 /note="internal transcribed spacer 1, (ITS1)" 237..391 /gene="5.8S rRNA" 237..391 /gene="5.8S rRNA" /product="5.8S ribosomal RNA" 392..>660 /note="internal transcribed spacer 2, (ITS2)"
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Best Local Similarity	99.1%; Pred. No. 1.3e-52;
Matches 231; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

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Db	4	ATAAAGTGTGAACAAGGTTTCCGTAGGTGAACCTCGGGAAGGATCATATTGAATGATA	63
QY	73	TAGAGTTGGTTGTCGCTCGCTCCCGGAGCATGTGCACGCTTCTCTTCATCCACAC	132
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QY	133	ACACCTGTGCACCTGTGACACGAGGACCGTAAAAAAGTCTTCCGTCTATTAAACACAC	192
Db	124	ACACCTGTGCACCTGTGACGAGGACCGTAAAAAAGTCTTCCGTCTATTAAACACAC	183
QY	193	AAACCCCTTTGATTAAATTGAATGATATTGATTAACGATCTCTTAAACT	245
Db	184	AAACCCCTTTGATTAAATTGAATGATATTGATTAACGATCTCTTGAACCT	236

RESULT 8	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
RSP242886	RSE242886	Rhizoctonia sp. Fab-S6 661 bp DNA linear	AJ242886	AJ242886.1	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.	Rhizoctonia sp. Fab-S6	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.

TITLE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL REFERENCE	Unpublished 2 (bases 1 to 661)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnología Microbiana, Centro Nacional de Biotecnología, Campus Cantoblanco, Universidad Autónoma de Madrid, Madrid 28049, SPAIN
FEATURES	
source	Location/Qualifiers 1..661

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Qy	74	AGAGTTGGTTGCTCGCTGCTCTCCGGAGAGATGTCAGCGCTTCTCTTTTCATCCACACA	133
Db	66	AGAGTTGGTTGCTCGCTGCTCTCCGGAGAGATGTCAGCGCTTCTCTTTTCATCCACACA	125

Qy	134	CATGTCGTCACCTTGTGGAGCGAGSAGACCGTAAAAAGCTTCGCTATTTAAACACACA	133
Db	126	CACGCTGCACCTTGTGACGCGSAGSACCGTAAAAAGCTTCGCTATTTAAACACACA	185
Qy	194	AAACCCATGTGATTTAAATTAATGTATTTATGATTAACGCATCTTTAAACT	245
Db	186	AAACCCATGTGATTTAAATTAATGTATTTATGATTAACGCATCTTTGAACCT	237

RESULT 9	RSP242881	665 bp	DNA	linear	PLN 15-JAN-2002
LOCUS	RSP242881				
DEFINITION	RSP242881 Rhizoctonia sp. Fab-S1 5.8S rRNA gene and ITS1 and 2, strain Fab-S1.				
ACCESSION	AJ242881				
VERSION	AJ242881.1	GI:18181603			
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.				
SOURCE	Rhizoctonia sp. Fab-S1.				
ORGANISM	Rhizoctonia sp. Fab-S1.				

FEATURES	REFERENCE
AUTHORS	1
TITLE	Salazar O., Munoz R., Lopez-Corcoles H. and Rubio V. Molecular characterization and pathogenicity of a new group of isolates of blinucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 665)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnología Microbiana, Centro Nacional de Biotecnología, Campus Cantoblanco, Universidad Autónoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers

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ORIGIN	

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Best Local Similarity	99.1%	Pred. No. 6e-49		
Matches 228	Conservative 0	Mismatches 1	Indels 1	Gaps 1

[illegible]

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
RESULT 10 RSP242897														
LOCUS	RSP242897	659 bp	DNA	linear	PLN 15-JAN-2002									
DEFINITION	Rhizoctonia sp. C-653	5.8S rRNA	gene and ITS1 and 2	strain C-653.										
ACCESSION	AJ242897													
VERSION	AJ242897.1	GI:18181854												
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 2; ITS1; ITS2.													
SOURCE														
ORGANISM	Rhizoctonia sp. C-653.													
REFERENCE	1													
AUTHORS	Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.													
TITLE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain													
JOURNAL	Unpublished													
REFERENCE	2 (bases 1 to 659)													
AUTHORS	Julian, M.C.													
TITLE	Direct Submission													
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN													
FEATURES	Location/Qualifiers													
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	/country="Spain"													
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BASE COUNT	178 a 131 c 143 g 207 t													
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Matches	219; Conservative 0; Mismatches 20; Indels 3; Gaps 3;													
OY	5 AGGGAGTAATAAAAGTCGTACAAAGGTTCCGTAGGTGACCTGCGGAAGGATCATATTG 64													
DB	13 AGAGAGAACTAAAGCTGTACAAAGGTTCCGTAGGTGACCTGCGGAAGGATCATATTG 72													
OY	65 AATGAATGTAGAGTTGGTTGCTGCGCTGCTC-CTCCGGAGCATGTGCACGCTTCTCTTT 123													
DB	73 AATGAATGTAGAGTTGGTTGCTGCGCTGCTC-CTCCGGAGCATGTGCACGCTTCTCTTT 132													

ACCESSION	AJ242898	GI:18181855	
VERSION	AJ242898.1		
KEYWORDS	5.8S ribosomal RNA, 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.		
SOURCE			
ORGANISM	Rhizoctonia sp. AV-2.		
REFERENCE			
AUTHORS	Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.		
TITLE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 661)		
AUTHORS	Julian, M.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbioliana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN		
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Best Local Similarity	88.5%; Pred. No. 3.5e-35;		
Matches 215; Conservative	0; Mismatches 23; Indels 5; Gaps 3;		
QY	5	AGGGAGTAATAAAGTCGTACAGAGTTTCCTCGTAGTGAACCTGGGAGAGATCATTTATG	64
Db	12	AGAGGAAGTAAAGTCGTACAGAGTTTCCTCGTAGTGAACCTGGGAGAGATCATTTATG	71
QY	65	AATGAATTAAGTTGGTGTGCTGCGTCTCT - -CCGGAGCATGTGACGCTTCTCT	122
Db	72	AATGAAGTAAAGTTGGTGTGCTGCGTCTCT - -CCGGAGCATGTGACGCTTCTCT	131
QY	123	TCATCCACACACACCTGTGCACTGTGTGACGAGAGACGTAATAAAGCTTCCGCTAT	182
Db	132	TCATCCACACACACCTGTGCACTGTGTGACGAGAG -GCTTTAATTAAGTCTTCGCTAC	190
QY	183	TAAACACACAAACCCCATGTGATTTAATTGAATGATTAATTGATGTAACGATCATTTAAA	242
Db	191	TTAATCACACAAAC -ATTTAATTAATTAATGAATGATTAATGATTAACGATCATTTAGA	248
QY	243	ACT 245	
Db	249	ACT 251	
RESULT 12			
RSP242899			
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DEFINITION	Rhizoctonia sp. 184 5.8S rRNA gene and ITS1 and 2, strain 184.		
ACCESSION	AJ242899		
VERSION	AJ242899.1	GI:18181856	
KEYWORDS	5.8S ribosomal RNA, 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.		
SOURCE			
ORGANISM	Rhizoctonia sp. 184.		

ORGANISM	Rhizoctonia sp. 184
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomyces;
AUTHORS	Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
TITLE	Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
JOURNAL	1 Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
REFERENCE	Molecular characterization and pathogenicity of a new group of
AUTHORS	isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.)
TITLE	isolated in Spain
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 661)
AUTHORS	Julian, M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biocologia
REFERENCE	Microbiologia, Centro Nacional de Biotecnologia, Campus Cantolabiano,
AUTHORS	Universidad Autonoma de Madrid, Madrid 28049, SPAIN
TITLE	Location/Qualifiers
JOURNAL	1.. 661
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AUTHORS	/strain="184"
TITLE	/db_xref="taxon:183702"
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TITLE	252.. 406
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JOURNAL	407.. >661
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AUTHORS	BASE COUNT 184 a 134 c 140 g 203 t
TITLE	ORIGIN
JOURNAL	Query Match 67.8%; Score 166.2; DB 8; Length 661;
REFERENCE	Best Local Similarity 88.5%; Pred. No. 3.5e-35;
AUTHORS	Matches 215; Conservative 0; Mismatches 23; Indels 5; Gaps 3;
TITLE	5 AGGGAAATAAAGTCGTACAAGGTTCCGTAGTGGAACCTCGGAAGATCATTAATG 64
JOURNAL	12 AGAGAGAATAAAGTCGTACAAGGTTCCGTAGTGGAACCTCGGAAGATCATTAATG 71
REFERENCE	65 AATGAATATAGAGTGTGCTGCCTGCCCT--CCGGAGCATGTGCACGCTTCTCTT 122
AUTHORS	72 AATGAACATAGAGTGTGCTGCCTGCCCTCCCTCACTGGGCGCATGTGCACGCTTCTCTT 131
TITLE	-OY 123 TCATCCACACACACTGTGCCTGTGTGAGAGCGAGAGACCGTAANAAGCTTCGCTCAT 182
JOURNAL	132 TCATCCACACACACTGTGCCTGTGTGAGAGCGAGAG--GCTTAATTAATGATCGCTCTAC 190
REFERENCE	OY 183 TAAACCACACAACCCATTGTATTAAATTAAGTAGTAATGATGTAACGCATCAATTAA 242
AUTHORS	Db 191 TTAATCACACAACGC--ATTTAATTAATTAATGATGTAATGATGTAACGCATCAATTAGA 248
TITLE	OY 243 ACT 245
JOURNAL	Db 249 ACT 251
REFERENCE	RESULT 13
AUTHORS	RSP242892
TITLE	LOCUS RSP242892 661 bp DNA linear PLN 15-JAN-2002
JOURNAL	DEFINITION Rhizoctonia sp. SIR-2 5.8S rRNA gene and ITS1 and 2, strain SIR-2.
REFERENCE	ACCESSION AJ242892
AUTHORS	VERSION AJ242892.1 GI:18181849
TITLE	KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;
JOURNAL	internal transcribed spacer 2; ITS1; ITS2.
REFERENCE	SOURCE Rhizoctonia sp. SIR-2.
AUTHORS	ORGANISM Eukaryota; Fungi; Basidiomycota; Hymenomyces;
TITLE	Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
JOURNAL	Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
REFERENCE	1

FEATURES	source
JOURNAL	Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
REFERENCE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
AUTHORS	Unpublished
TITLE	2 (bases 1 to 661)
JOURNAL	Julian, M.C.
REFERENCE	Direct Submission
AUTHORS	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
TITLE	Location/Qualifiers
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REFERENCE	Best Local Similarity 80.4%; Pred. No. 4.3e-29;
AUTHORS	Matches 193; Conservative 0; Mismatches 45; Indels 2; Gaps 2;
TITLE	QY 5 AGGGGATAATAAAAGTCTAGACAGGTTTCCGTAGCTGACCTGGGAAGATCATATTG 64
JOURNAL	15 AGAGAGAGTAAAGTCGTACACAGGTTCCGTAGGTGACCTGGGAAGATCATATTG 74
REFERENCE	QY 65 AATGAATATAGAGTTGGTTGCTGCTGCT-CCTCCGGAGCATGTGCAGCGTTTCTCT-T 122
AUTHORS	DB 75 AATGAACCTTAGTGCTGGTGGCTGGCTGCTGCTTTGGCAGCATGTGCAGCGCTTCTCTAT 134
TITLE	QY 123 TCATCCACACACACTGTGCACCTGTGAGAGGAGGAGCAATAAAAGTCTTCGCTCAT 182
JOURNAL	DB 135 TCATCCACACACCCCTGTGCACCTGTGAGACTGGAGCCGTAATAAGCCTTCAGTCTGCT 194
REFERENCE	QY 183 TAACACACAAACCCCATTTGTTTAAATTTGAATGTATTTGATGATTAAGCATTAATAA 242
AUTHORS	DB 195 AAATTCATATACAAACGTCATTTAAATTGAACGTGAATGTACTTGATGTAAAGCATCATTA 254
TITLE	RESULT 14
JOURNAL	RSP242902
REFERENCE	LOCUS Rhizoctonia sp. TC1 5.8S rRNA gene and ITS1 and 2, strain TC1. 694 bp DNA linear PLN 15-JAN-2002
AUTHORS	DEFINITION AJ242902.1 GI:18181859
TITLE	VERSION AJ242902.1 GI:18181859
JOURNAL	KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
REFERENCE	SOURCE Rhizoctonia sp. TC1
AUTHORS	ORGANISM Rhizoctonia sp. TC1
TITLE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Ceratobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; Ceratobasidiaceae; Rhizoctonia.
JOURNAL	Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
REFERENCE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
AUTHORS	Unpublished
TITLE	2 (bases 1 to 694)
JOURNAL	Julian, M.C.
REFERENCE	Direct Submission
AUTHORS	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia

Microbiana, Centro Nacional de Biotecnología, Campus Cantoblanco,  
Universidad Autónoma de Madrid, Madrid 28049, SPAIN

## FEATURES

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65 AATGAATATAGAGTTGTTGCTGCTGCT-CCTCCGGAGCATGTGCACGCTTTCTC-TT 122

72 AATGAATATAGAGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131

123 TCATCCACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182

132 TCATCCACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191

183 TAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 241

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242 A 242

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Db

## RESULT 15

RSP242893

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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AUTHORS

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REFERENCE

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REFERENCE

AUTHORS

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JOURNAL

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/country="Spain"

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/note="internal transcribed spacer 1, (ITS1)"

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BASE COUNT 179 a 141 c 141 g 200 t

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Query Match 57.5% Score 140.8; DB 8; Length 661;

Best Local Similarity 79.6% Pred. No. 3.3e-28; Mismatches 47; Indels 2; Gaps 2;

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15 AGAGGAAGTAAGTCGTACAGAGTTCCGTAGGTGAACCTCGGAAGATCATTTATG 74

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75 AATGAATATAGAGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 134

123 TCATCCACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182

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183 TAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 242

195 AATTCATATCAAAACCATTTAATGAACTGATGATGATGATGATGATGATGAT 254

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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 05:44:08 ; Search time 129 Seconds  
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Sequence: 1 tttagaggggaataaagc.....tgaacgcatactaaact 245

Scoring table: IDENTITY\_NUC  
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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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18: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	100.0	400	21	AAZ92450 Rhizoctonia sp. is
2	238.6	97.4	401	21	AAZ92451 Rhizoctonia sp. is
3	235.4	96.1	407	21	AAZ92452 Rhizoctonia sp. is
4	234.6	95.8	398	21	AAZ92446 Rhizoctonia sp. is
5	231.6	94.5	393	21	AAZ92447 Rhizoctonia sp. is
6	231.4	94.4	405	21	AAZ92445 Rhizoctonia sp. is
7	229.8	93.8	391	21	AAZ92448 Rhizoctonia sp. is
8	225.6	92.1	392	21	AAZ92449 Rhizoctonia sp. is
9	216.4	88.3	385	21	AAZ92453 Rhizoctonia sp. is

10	173	70.6	408	21	AAZ92468 Rhizoctonia sp. is
11	166.2	67.8	406	21	AAZ92467 Rhizoctonia sp. is
12	144	58.8	411	21	AAZ92465 Rhizoctonia sp. is
13	142.6	58.2	409	21	AAZ92463 Rhizoctonia sp. is
14	140.8	57.5	411	21	AAZ92466 Rhizoctonia sp. is
15	133.6	54.5	410	21	AAZ92464 Rhizoctonia sp. is
16	128	52.2	385	21	AAZ92460 Rhizoctonia sp. is
17	122	49.8	381	21	AAZ92455 Rhizoctonia sp. is
18	117.2	47.8	412	21	AAZ92469 Rhizoctonia sp. is
19	116.2	47.4	394	21	AAZ92458 Rhizoctonia sp. is
20	114.8	46.9	387	21	AAZ92454 Rhizoctonia sp. is
21	112	45.7	415	21	AAZ92472 Rhizoctonia sp. is
22	106.2	43.3	415	21	AAZ92473 Rhizoctonia sp. is
23	105	42.9	413	21	AAZ92470 Rhizoctonia sp. is
24	104.8	42.8	416	21	AAZ92462 Rhizoctonia sp. is
25	103.4	42.2	413	21	AAZ92471 Rhizoctonia sp. is
26	98.2	40.1	414	21	AAZ92475 Rhizoctonia sp. is
27	92.4	37.7	416	21	AAZ92474 Rhizoctonia sp. is
28	84.6	34.5	328	21	AAZ92459 Rhizoctonia sp. is
29	83.8	34.2	684	22	AAZ92458 Internal transcrib
30	80.6	32.9	685	22	AAZ92457 Internal transcrib
31	72.8	29.7	686	22	AAZ92456 Internal transcrib
32	69.6	28.4	686	22	AAZ92455 Internal transcrib
33	69.6	28.4	686	22	AAZ92454 Internal transcrib
34	69.6	28.4	686	22	AAZ92453 Internal transcrib
35	69.6	28.4	687	22	AAZ92452 Internal transcrib
36	69.6	28.4	687	22	AAZ92451 Internal transcrib
37	69.6	28.4	687	22	AAZ92450 Internal transcrib
38	69.6	28.4	687	22	AAZ92449 Internal transcrib
39	69.6	28.4	687	22	AAZ92448 Internal transcrib
40	68.4	27.9	428	21	AAZ92457 Rhizoctonia sp. is
41	67.4	27.5	429	21	AAZ92456 Rhizoctonia sp. is
42	62.4	25.5	375	22	AAZ92482 DNA sequence from
43	60.8	24.8	357	21	AAZ92483 Rhizoctonia sp. is
44	57	23.3	253	22	AAZ92493 Nucleic acid diffe
45	55.2	22.5	3420	24	ABA99033 Saccharomyces cere

#### ALIGNMENTS

RESULT 1	AAZ92450	standard; DNA; 400 BP.
ID	AAZ92450	
XX	AAZ92450:	
AC	05-JUN-2000	(first entry)
XX		
DT		
XX	Rhizoctonia sp. isolate Eab-F1 ribosomal DNA, ITS1-5.8s region.	
DE		
XX		
KW	Antifungal; biocontrol; binucleate; non-pathogenic fungus;	
KW	Strain identification; classification; internal transcribed spacer;	
KW	ITS region; 5.8s region; ribosomal; ds.	
XX		
OS	Rhizoctonia sp.	
XX		
PN	WO200004779-A1.	
XX		
PD	03-FEB-2000.	
XX		
PF	23-JUL-1999;	99WO-GB02406.
XX		
PR	24-JUL-1998;	98GB-0016265.
XX		
PA	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.	
PA	(RUEF/) RUEFLES G K.	
XX		
PI	Rubio Susan V, Salazar Torres O, Julian Esquivias M;	
PI	Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;	
PI	Lopez Corcoles H;	
XX		
DR	WPI; 2000-182492/16.	

XX Protection of plants including tomato, pepper, lettuce, radish,  
PT parsley, sugar beet, rape, and onions against pathogenic fungi, uses a  
PT binucleate Rhizoctonia strain for biocontrol -  
PS Claim 5; Fig 1; 121pp; English.  
XX  
CC The invention relates to a novel method of protecting plants from  
CC pathogenic fungi. The method comprises biocontrol of pathogenic fungi  
CC via the use of a non-pathogenic, binucleate Rhizoctonia strain. The  
CC binucleate Rhizoctonia is selected by molecular detection of certain  
CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences  
CC (AA292445-AA292458), which vary between strains of these fungi. The  
CC invention also encompasses a concentrate for use in plant protection  
CC containing viable material from the binucleate Rhizoctonia strains of the  
CC invention, and primers (AA292437-292444) for identifying these strains.  
CC The strains of the invention are used as biocontrol agents for related  
CC pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for  
CC its ability to protect tomato seedlings from the pathogenic Rhizoctonia  
CC strain Me8.2. The Rhizoctonia strains were inoculated either  
CC simultaneously or consecutively (the binucleate strain followed by the  
CC pathogenic strain), and the protection effect indicated by the degree of  
CC infected vegetal surface. The binucleate strain was found to provide  
CC protection against the pathogenic strain when it had been allowed to  
CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,  
CC consecutive inoculation), whereas no protection was provided when both  
CC strains were inoculated simultaneously. The method of the invention may  
CC be used to protect a wide variety of plants from pathogenic fungal  
CC infection. Plants that may be protected include vegetables, crops such as  
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The  
CC method is reliable and provides economical biocontrol of diseases caused  
CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s  
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic  
CC binucleate Rhizoctonia strains of the invention.  
XX  
SQ Sequence 400 BP; 116 A; 83 C; 88 G; 113 T; 0 other;  
Query Match 100.0%; Score 245; DB 21; Length 400;  
Best Local Similarity 100.0%; Pred. No. 3; 8e-71;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTAGAGGGGAATAAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 60  
DB 1 TTAGAGGGGAATAAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 60  
QY 61 ATTGAATGAATATAGAGTTGCTGCTGCTCCGCGGAGCATGTGCACGCTTTCTC 120  
DB 61 ATTGAATGAATATAGAGTTGCTGCTGCTCCGCGGAGCATGTGCACGCTTTCTC 120  
QY 121 TTTTCATCCACACACCTGTGCACCTGTGAGACGAGGACCGTAATAAAGTCTCCGTCT 180  
DB 121 TTTTCATCCACACACCTGTGCACCTGTGAGACGAGGACCGTAATAAAGTCTCCGTCT 180  
QY 181 ATTAACCAACCAACCCCATTTGATTTAAATTGAATGTAATGTAACGCATCATTA 240  
DB 181 ATTAACCAACCAACCCCATTTGATTTAAATTGAATGTAATGTAACGCATCATTA 240  
QY 241 AAACCT 245  
DB 241 AAACCT 245  
RESULT 2  
AA292451  
ID AA292451 standard; DNA: 401 BP.  
XX AA292451;  
AC  
XX  
DT 05-JUN-2000 (first entry)  
XX Rhizoctonia sp. isolate Eab-F6 ribosomal DNA, ITS1-5.8s region.  
XX  
KW Antifungal; biocontrol; binucleate; non-pathogenic fungus;

KW strain identification; classification; internal transcribed spacer;  
KW ITS region: 5.8s region; ribosomal; ds.  
XX  
XX Rhizoctonia sp.  
OS  
XX  
XX WO200004779-A1.  
PN  
XX  
PD 03-FEB-2000.  
XX  
XX 23-JUL-1999; 99WO-GB02406.  
PF  
XX  
PR 24-JUL-1998; 98GB-0016265.  
PA (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.  
PA (RUFFE) RUFFLES G K.  
XX  
XX Rubio Susan V, Salazar Torres O, Julian Esquivias M,  
PI Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;  
PI Lopez Corcoles H;  
XX  
DR WPI: 2000-182492/16.  
XX  
PT Protection of plants including tomato, pepper, lettuce, radish,  
PT parsley, sugar beet, rape, and onions against pathogenic fungi, uses a  
PT binucleate Rhizoctonia strain for biocontrol -  
XX  
PS Claim 5; Fig 1; 121pp; English.  
XX  
CC The invention relates to a novel method of protecting plants from  
CC pathogenic fungi. The method comprises biocontrol of pathogenic fungi  
CC via the use of a non-pathogenic, binucleate Rhizoctonia strain. The  
CC binucleate Rhizoctonia is selected by molecular detection of certain  
CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences  
CC (AA292445-AA292458), which vary between strains of these fungi. The  
CC invention also encompasses a concentrate for use in plant protection  
CC containing viable material from the binucleate Rhizoctonia strains of the  
CC invention, and primers (AA292437-292444) for identifying these strains.  
CC The strains of the invention are used as biocontrol agents for related  
CC pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for  
CC its ability to protect tomato seedlings from the pathogenic Rhizoctonia  
CC strain Me8.2. The Rhizoctonia strains were inoculated either  
CC simultaneously or consecutively (the binucleate strain followed by the  
CC pathogenic strain), and the protection effect indicated by the degree of  
CC infected vegetal surface. The binucleate strain was found to provide  
CC protection against the pathogenic strain when it had been allowed to  
CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,  
CC consecutive inoculation), whereas no protection was provided when both  
CC strains were inoculated simultaneously. The method of the invention may  
CC be used to protect a wide variety of plants from pathogenic fungal  
CC infection. Plants that may be protected include vegetables, crops such as  
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The  
CC method is reliable and provides economical biocontrol of diseases caused  
CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s  
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic  
CC binucleate Rhizoctonia strains of the invention.  
XX  
SQ Sequence 401 BP; 116 A; 83 C; 88 G; 114 T; 0 other;  
Query Match 97.4%; Score 238.6; DB 21; Length 401;  
Best Local Similarity 98.4%; Pred. No. 5e-69;  
Matches 241; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TTAGAGGGGAATAAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 60  
DB 2 TTAGAGGGGAATAAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 61  
QY 61 ATTGAATGAATATAGAGTTGCTGCTGCTCCGCGGAGCATGTGCACGCTTTCTC 120  
DB 62 ATTGAATGAATATAGAGTTGCTGCTGCTCCGCGGAGCATGTGCACACATTTCTC 121  
QY 121 TTTTCATCCACACACCTGTGCACCTGTGAGACGAGGACCGTAATAAAGTCTCCGTCT 180  
DB 122 TTTTCATCCACACACCTGTGCACCTGTGAGACGAGGACCGTAATAAAGTCTCCGTCT 181





AA292445;  
 05-JUN-2000 (first entry)  
 Rhizoctonia sp. isolate Eab-F2 ribosomal DNA, ITS1-5.8s region.  
 Antifungal; biocontrol; binucleate; non-pathogenic fungus;  
 strain identification; classification; internal transcribed spacer;  
 ITS region; 5.8s region; ribosomal; ds.  
 Rhizoctonia sp.  
 W0200004779-A1.  
 03-FEB-2000.  
 23-JUL-1999; 99WO-GB02406.  
 24-JUL-1998; 98GB-0016265.  
 (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.  
 (RUFEL) RUFLES G K.  
 Rubio Susan V, Salazar Torres O, Julian Esquivias M;  
 Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;  
 Lopez Corcoles H;  
 WPI: 2000-182492/16.  
 Protection of plants including tomato, pepper, lettuce, radish,  
 parsley, sugar beet, rape, and onions against pathogenic fungi, uses a  
 binucleate Rhizoctonia strain for biocontrol -  
 Claim 5; Fig 1; 121pp; English.

The invention relates to a novel method of protecting plants from  
 pathogenic fungi. The method comprises biocontrol of pathogenic fungi  
 via the use of a non-pathogenic, binucleate Rhizoctonia strain. The  
 binucleate Rhizoctonia is selected by molecular detection of certain  
 internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences  
 (AA292445-AA292458), which vary between strains of these fungi. The  
 invention also encompasses a concentrate for use in plant protection  
 containing viable material from the binucleate Rhizoctonia strains of the  
 invention, and primers (AA292437-292444) for identifying these strains.  
 The strains of the invention are used as biocontrol agents for related  
 pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for  
 its ability to protect tomato seedlings from the pathogenic Rhizoctonia  
 strain Me8.2. The Rhizoctonia strains were inoculated either  
 simultaneously or consecutively (the binucleate stain followed by the  
 pathogenic strain), and the protection effect indicated by the degree of  
 infected vegetal surface. The binucleate strain was found to provide  
 protection against the pathogenic strain when it had been allowed to  
 colonise the vegetal surface prior to pathogenic fungal infection (i.e.,  
 consecutive inoculation), whereas no protection was provided when both  
 strains were inoculated simultaneously. The method of the invention may  
 be used to protect a wide variety of plants from pathogenic fungal  
 infection. Plants that may be protected include vegetables, crops such as  
 oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The  
 method is reliable and provides economical biocontrol of diseases caused  
 by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s  
 regions of ribosomal RNA-encoding DNA from the novel non-pathogenic  
 binucleate Rhizoctonia strains of the invention.

Sequence 405 BP; 114 A; 83 C; 89 G; 111 T; 8 other;

Query Match 94.4%; Score 231.4; DB 21; Length 405;  
 Best Local Similarity 97.1%; Pred. No. 1.2e-66;  
 Matches 233; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 TTAGAGGGAATATAAAGTGTGTAACAAGCTTTCGTAAGTGAACCTGCGGAAGATCATT 60  
 : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5 DNNNAAGAGAAAGTAAGTGTGTAACAAGCTTTCGTAAGTGAACCTGCGGAAGATCATT 64

61 ATTGAATGAATATAGAGTGTGTGCTGCTGCTCCCGGAGAGATGTCACGCTTTCTC 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 65 ATTGAATGAATATAGAGTGTGTGCTGCTGCTCCCGGAGAGATGTCACGCTTTCTC 124  
 121 TTTTCATCCACACACACCTGTGCACTTTGTGAGACGAGACCGTAATAAAGTCTCCGTCT 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 125 TTTTCATCCACACACACCTGTGCACTTTGTGAGACGAGACCGTAATAAAGTCTCCGTCT 184  
 181 ATTAAACCAACAAACCCCATTTATTTAAATTGAATGTAATGTAACGATCATTA 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 185 ATTAAACCAACAAACCCCATTTATTTAAATTGAATGTAATGTAACGATCATTA 244

RESULT 7  
 AA292448  
 ID AA292448 standard; DNA; 391 BP.  
 XX  
 AA292448;  
 05-JUN-2000 (first entry)  
 Rhizoctonia sp. isolate Eab-S5 ribosomal DNA, ITS1-5.8s region.  
 Antifungal; biocontrol; binucleate; non-pathogenic fungus;  
 strain identification; classification; internal transcribed spacer;  
 ITS region; 5.8s region; ribosomal; ds.  
 Rhizoctonia sp.  
 W0200004779-A1.  
 03-FEB-2000.  
 23-JUL-1999; 99WO-GB02406.  
 24-JUL-1998; 98GB-0016265.  
 (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.  
 (RUFEL) RUFLES G K.  
 Rubio Susan V, Salazar Torres O, Julian Esquivias M;  
 Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;  
 Lopez Corcoles H;  
 WPI: 2000-182492/16.  
 Protection of plants including tomato, pepper, lettuce, radish,  
 parsley, sugar beet, rape, and onions against pathogenic fungi, uses a  
 binucleate Rhizoctonia strain for biocontrol -  
 Claim 5; Fig 1; 121pp; English.

The invention relates to a novel method of protecting plants from  
 pathogenic fungi. The method comprises biocontrol of pathogenic fungi  
 via the use of a non-pathogenic, binucleate Rhizoctonia strain. The  
 binucleate Rhizoctonia is selected by molecular detection of certain  
 internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences  
 (AA292445-AA292458), which vary between strains of these fungi. The  
 invention also encompasses a concentrate for use in plant protection  
 containing viable material from the binucleate Rhizoctonia strains of the  
 invention, and primers (AA292437-292444) for identifying these strains.  
 The strains of the invention are used as biocontrol agents for related  
 pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for  
 its ability to protect tomato seedlings from the pathogenic Rhizoctonia  
 strain Me8.2. The Rhizoctonia strains were inoculated either  
 simultaneously or consecutively (the binucleate stain followed by the  
 pathogenic strain), and the protection effect indicated by the degree of  
 infected vegetal surface. The binucleate strain was found to provide  
 protection against the pathogenic strain when it had been allowed to  
 colonise the vegetal surface prior to pathogenic fungal infection (i.e.,  
 consecutive inoculation), whereas no protection was provided when both  
 strains were inoculated simultaneously. The method of the invention may  
 be used to protect a wide variety of plants from pathogenic fungal

CC Infection. Plants that may be protected include vegetables, crops such as  
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The  
CC method is reliable and provides economical biocontrol of diseases caused  
CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s  
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic  
CC binucleate Rhizoctonia strains of the invention.

XX Sequence 391 BP; 110 A; 83 C; 86 G; 112 T; 0 other;

Query Match 93.8%; Score 229.8; DB 21; Length 391;  
Best Local Similarity 99.1%; Pred. No. 4.1e-66;  
Matches 231; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 AAAAGTCGTAAACAGGTTTCCGTAGTGAACCTGCGGAGAGATCATTTGAATGAATA 72  
DB 4 ATAAAGTCGTAAACAGGTTTCCGTAGTGAACCTGCGGAGAGATCATTTGAATGAATA 63  
QY 73 TAGAGTTGGTGTGCGCTGCTCCCGGAGAGATGTCACGCTTCTCTTCATCCACAC 132  
DB 64 TAGAGTTGGTGTGCGCTGCTCCCGGAGAGATGTCACGCTTCTCTTCATCCACAC 123  
QY 133 ACACCTGTGCACTGTGTAGAGGAGACCGTAAAAAGTCTTCGTATTAACACACAC 192  
DB 124 ACACCTGTGCACTGTGTAGAGGAGACCGTAAAAAGTCTTCGTATTAACACACAC 183  
QY 193 AAACCCCATTTGATTTAATTGAATGATTAATGATTAACGATCATTTAAACT 245  
DB 184 AAACCCCATTTGATTTAATTGAATGATTAATGATTAACGATCATTTAAACT 236

RESULT 8  
AA292449  
ID AA292449 standard; DNA; 392 BP.

XX AA292449;  
AC 05-JUN-2000 (first entry)  
DE Rhizoctonia sp. isolate Eab-s6 ribosomal DNA, ITS1-5.8s region.  
XX  
KW Antifungal; biocontrol; binucleate; non-pathogenic fungus;  
KW strain identification; classification; internal transcribed spacer;  
KW ITS region; 5.8s region; ribosomal; ds.  
XX OS Rhizoctonia sp.  
XX PN WO200004779-A1.  
XX PD 03-FEB-2000.  
XX PF 23-JUL-1999; 99WO-GB02406.  
XX PR 24-JUL-1998; 98GB-0016265.  
PA (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.  
PA (RUFF/) RUFFLES G K.  
XX PI Rubio Susan V, Salazar Torres O, Julian Esquivias M,  
PI Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;  
PI Lopez Corcoles H;  
XX DR WPI: 2000-182492/16.  
XX PT Protection of plants including tomato, pepper, lettuce, radish,  
PT parsley, sugar beet, rape, and onions against pathogenic fungi, uses a  
PT binucleate Rhizoctonia strain for biocontrol -  
XX PS Claim 5; Fig 1; 121pp; English.

CC The invention relates to a novel method of protecting plants from  
CC pathogenic fungi. The method comprises biocontrol of pathogenic fungi  
CC via the use of a non-pathogenic, binucleate Rhizoctonia strain. The  
CC binucleate Rhizoctonia is selected by molecular detection of certain

CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences  
CC (AA292445-AA292458), which vary between strains of these fungi. The  
CC invention also encompasses a concentrate for use in plant protection  
CC containing viable material from the binucleate Rhizoctonia strains of the  
CC invention, and primers (AA292437-292444) for identifying these strains.  
CC The strains of the invention are used as biocontrol agents for related  
CC pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for  
CC its ability to protect tomato seedlings from the pathogenic Rhizoctonia  
CC strain Me8.2. The Rhizoctonia strains were inoculated either  
CC simultaneously or consecutively (the binucleate strain followed by the  
CC pathogenic strain), and the protection effect indicated by the degree of  
CC infected vegetal surface. The binucleate strain was found to provide  
CC protection against the pathogenic strain when it had been allowed to  
CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,  
CC consecutive inoculation), whereas no protection was provided when both  
CC strains were inoculated simultaneously. The method of the invention may  
CC be used to protect a wide variety of plants from pathogenic fungal  
CC infection. Plants that may be protected include vegetables, crops such as  
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The  
CC method is reliable and provides economical biocontrol of diseases caused  
CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s  
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic  
CC binucleate Rhizoctonia strains of the invention.

XX Sequence 392 BP; 110 A; 83 C; 89 G; 110 T; 0 other;

Query Match 92.1%; Score 225.6; DB 21; Length 392;  
Best Local Similarity 98.3%; Pred. No. 1e-64;  
Matches 228; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 14 AAAAGTCGTAAACAGGTTTCCGTAGTGAACCTGCGGAGAGATCATTTGAATGAATA 73  
DB 6 AAAAGTCGTAAACAGGTTTCCGTAGTGAACCTGCGGAGAGATCATTTGAATGAATA 65  
QY 74 AGAGTTGGTGTGCGCTGCTCCCGGAGAGATGTCACGCTTCTCTTCATCCACACA 133  
DB 66 AGAGTTGGTGTGCGCTGCTCCCGGAGAGATGTCACGCTTCTCTTCATCCACACA 125  
QY 134 CACCTGTGCACTGTGTAGAGGAGACCGTAAAAAGTCTTCGTATTAACACACACA 193  
DB 126 CACCTGTGCACTGTGTAGAGGAGACCGTAAAAAGTCTTCGTATTAACACACACA 185  
QY 194 AAACCCCATTTGATTTAATTGAATGATTAATGATTAACGATCATTTAAACT 245  
DB 186 AAACCCCATTTGATTTAATTGAATGATTAATGATTAACGATCATTTAAACT 237

RESULT 9  
AA292453  
ID AA292453 standard; DNA; 385 BP.

XX AA292453;  
AC 05-JUN-2000 (first entry)  
DE Rhizoctonia sp. isolate Eab-s1 ribosomal DNA, ITS1-5.8s region.  
XX  
KW Antifungal; biocontrol; binucleate; non-pathogenic fungus;  
KW strain identification; classification; internal transcribed spacer;  
KW ITS region; 5.8s region; ribosomal; ds.  
XX OS Rhizoctonia sp.  
XX PN WO200004779-A1.  
XX PD 03-FEB-2000.  
XX PF 23-JUL-1999; 99WO-GB02406.  
XX PR 24-JUL-1998; 98GB-0016265.  
PA (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.  
PA (RUFF/) RUFFLES G K.

xx	Rubio Susan V, Salazar Torres O, Julian Esquivias M;
pi	Gonzales Garcia V, Gomez Acebo Gullon E, Munoz Gomez R;
pi	Lopez Corcoles H;
xx	WP1: 2000-182492/16.
DR	
xx	
xx	Protection of plants including tomato, pepper, lettuce, radish,
PT	parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
PT	binucleate Rhizoctonia strain for biocontrol .
xx	
PS	Claim 5; Fig 1; 121pp; English.
xx	
CC	The invention relates to a novel method of protecting plants from
CC	pathogenic fungi. The method comprises biocontrol of pathogenic fungi
CC	via the use of a non-pathogenic, binucleate Rhizoctonia strain. The
CC	binucleate Rhizoctonia is selected by molecular detection of certain
CC	internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC	(AA929445-292458), which vary between strains of these fungi. The
CC	invention also encompasses a concentrate for use in plant protection
CC	containing viable material from the binucleate Rhizoctonia strains of the
CC	invention, and primers (AA929437-292444) for identifying these strains.
CC	The strains of the invention are used as biocontrol agents for related
CC	pathogenic fungi. Binucleate Rhizoctonia isolate Bab-F2 was tested for
CC	its ability to protect tomato seedlings from the pathogenic Rhizoctonia
CC	strain Me8.2. The Rhizoctonia strains were inoculated either
CC	simultaneously or consecutively (the binucleate strain followed by the
CC	pathogenic strain), and the protection effect indicated by the degree of
CC	infected vegetal surface. The binucleate strain was found to provide
CC	protection against the pathogenic strain when it had been allowed to
CC	colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
CC	consecutive inoculation), whereas no protection was provided when both
CC	strains were inoculated simultaneously. The method of the invention may
CC	be used to protect a wide variety of plants from pathogenic fungal
CC	infection. Plants that may be protected include vegetables, crops such as
CC	oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC	method is reliable and provides economical biocontrol of diseases caused
CC	by Rhizoctonia solani. Sequences AA929445-292458 represent the ITS-5.8s
CC	regions of Rhizoctonia RNA-encoding DNA from the novel non-pathogenic
CC	binucleate Rhizoctonia strains of the invention.
xx	
SQ	Sequence 385 BP; 107 A; 83 C; 85 G; 110 T; 0 other;
	Query Match 88.3%; Score 216.4; DB 21; Length 385;
	Best Local Similarity 99.1%; Pred. No. 1.1e-61;
	Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1.
QY	17 AGTCGTAAACAAGGTTCCGTAGGTAAACCTCGCGAAGGATCATTTTGGATGAATATAGA 76
Db	1 AGCTGTACAAGGTTCCGTAGGTAAACCTCGCGAAGGATCATTTTGAATTAATATAGA 60
QY	77 GTTGCTTTCCGTGGCTCCTC-CGGAGACATGTGCACGCTTCTCTTCATCCACACACA 135
Db	61 GTTGCTTTCCGTGGCTCCTCCTCGGGAGACATGTGCACGCTTCTCTTCATCCACACACA 120
QY	136 CCTGTGCACTTGTGAGACGAGACCGTAAAAAAGCTTCCTCGTAAATTAAACACACAAA 195
Db	121 CCTGTGCACTTGTGAGACGAGACCGTAAAAAAGCTTCCTCTTAATTAAACACACAAA 180
QY	196 CCCCATTTGATTTAAATTGAATGTAAATTGATGTAAACGATCATTTAAACT 245
Db	181 CCCCATTTGATTTAAATTGAATGTAAATTGATGTAAACGATCATTTGAAGT 230
RESULT 10	
AA929468	
ID	AA929468 standard; DNA: 408 BP.
xx	
AC	AA929468;
xx	
DT	05-JUN-2000 (first entry)
xx	
DE	Rhizoctonia sp. isolate AGC ribosomal DNA, ITS1-5.8s region.

XX	Antifungal; biocontrol; binucleate; non-pathogenic fungus;
KW	strain identification; classification; internal transcribed spacer;
KW	ITS region; 5.8s region; ribosomal; ds.
XX	
OS	Rhizoctonia sp.
PN	MO200004779-AL.
PD	03-FEB-2000.
PF	23-JUL-1999; 99MO-GH02406.
XX	
PR	24-JUL-1998; 98GB-0016265.
XX	
PA	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.
PA	(RUFF/) RUFFLES G K.
XX	
PI	Rubio Susan V, Salazar Torres O, Julian Esquivias M;
PI	Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
XX	Lopez Corcoles H;
PI	WPI: 2000-182492/16.
XX	
PT	Protection of plants including tomato, pepper, lettuce, radish,
PT	parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
PT	binucleate Rhizoctonia strain for biocontrol -
XX	
PS	Disclosure; Fig 1; 121pp; English.
XX	
CC	The invention relates to a novel method of protecting plants from
CC	pathogenic fungi. The method comprises biocontrol of pathogenic fungi
CC	via the use of a non-pathogenic, binucleate Rhizoctonia strain. The
CC	binucleate Rhizoctonia is selected by molecular detection of certain
CC	internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC	(AA292443-AA292436), which vary between strains of these fungi. The
CC	invention also encompasses a concentrate for use in plant protection
CC	containing viable material from the binucleate Rhizoctonia strains of the
CC	invention, and primers (AA292437-292444) for identifying these strains.
CC	The strains of the invention are used as biocontrol agents for related
CC	pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for
CC	its ability to protect tomato seedlings from the pathogenic Rhizoctonia
CC	strain Me8.2. The Rhizoctonia strains were inoculated either
CC	simultaneously or consecutively (the binucleate strain followed by the
CC	pathogenic strain), and the protection effect indicated by the degree of
CC	infected vegetal surface. The binucleate strain was found to provide
CC	protection against the pathogenic strain when it had been allowed to
CC	colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
CC	consecutive inoculation), whereas no protection was provided when both
CC	strains were inoculated simultaneously. The method of the invention may
CC	be used to protect a wide variety of plants from pathogenic fungal
CC	infection. Plants that may be protected include vegetables, crops such as
CC	oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC	method is reliable and provides economical biocontrol of diseases caused
CC	by Rhizoctonia solani. Sequences AA292459-292490 represent the ITS-5.8s
CC	regions of ribosomal RNA encoding DNA from a variety of Rhizoctonia
CC	strains.
XX	
SO	Sequence 408 BP; 109 A; 84 C; 91 G; 124 T; 0 other;
XX	
Query Match	70.6%; Score 173; DB 21; Length 408;
Best Local Similarity	90.1%; Pred. No. 2.9e-47;
Matches 219; Conservative	0; Mismatches 20; Indels 4; Gaps 3
0Y	5 AGGGGAATAAAGTGTGTAACAAGTTCCTGATGGTGAACCTGGCGAAGATCATTTATG 64
Db	13 AGAGGAGTAAAGTGTGTAACAAGTTCCTGATGGTGAACCTGGCGAAGATCATTTATG 72
0Y	65 AATGAATATAGATTTGGTTGTGCGTGGCTCTT--CCGGGAGCATGTGACGCTTTCTCTT 122
Db	73 AATGAATGTGAGTGTGTGTGTGCGCTTGGCCCTTTACTGTGGGGTATGTGTGACGCCCTTCTT 132
0Y	123 TCATCCACACACACCTGTGCATCTTGTGAACGAGGACCGTAAATAAAGTCTCCGTAT 182

```
|||||
Db 133 TCATCCACACACACCTGCGACTGTGAGACGGAGG--GCTTTAATTAAGTCTCCGTAT 191
Oy 183 TAAACCCACAAACCCCATGTTATTTAATGATGTAATGATGTAACGATCATTTAA 242
Db 192 TCAACCCACACAAA--CTCATGTTATTTAACGATGTAATGATGTAACGATCATTTAGA 250
Oy 243 ACT 245
|||
Db 251 ACT 253

RESULT 11
AA292467
ID AA292467 standard; DNA: 406 BP.
AC AA292467;
XX
XX
XX 05-JUN-2000 (first entry)
XX
DE Rhizoctonia sp. isolate AGJ ribosomal DNA, ITS1-5.8s region.
XX
XX Antifungal; biocontrol; binucleate; non-pathogenic fungus;
XX strain identification; classification; internal transcribed spacer;
XX ITS region; 5.8s region; ribosomal; ds.
XX
XX Rhizoctonia sp.
XX
XX WO200004779-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-GB02406.
XX
XX 24-JUL-1998; 98GB-0016265.
XX
XX (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.
XX (RUFEL) RUFEL G K.
XX
XX Rubio Susan V, Salazar Torres O, Julian Esquivias M;
XX Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
XX Lopez Corcoles H;
XX
XX WPI: 2000-182492/16.
XX
XX Protection of plants including tomato, pepper, lettuce, radish,
XX parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
XX binucleate Rhizoctonia strain for biocontrol -
XX
XX Disclosure: Fig 1; 121pp; English.
XX
XX The invention relates to a novel method of protecting plants from
XX pathogenic fungi. The method comprises biocontrol of pathogenic fungi
XX via the use of a non-pathogenic, binucleate Rhizoctonia strain. The
XX binucleate Rhizoctonia is selected by molecular detection of certain
XX internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
XX (AA292445-AA292458), which vary between strains of these fungi. The
XX invention also encompasses a concentrate for use in plant protection
XX containing viable material from the binucleate Rhizoctonia strains of the
XX invention, and primers (AA292437-292444) for identifying these strains.
XX The strains of the invention are used as biocontrol agents for related
XX pathogenic fungi. Binucleate Rhizoctonia isolate Bab-F2 was tested for
XX its ability to protect tomato seedlings from the pathogenic Rhizoctonia
XX strain Me8.2. The Rhizoctonia strains were inoculated either
XX simultaneously or consecutively (the binucleate strain followed by the
XX pathogenic strain), and the protection effect indicated by the degree of
XX infected vegetal surface. The binucleate strain was found to provide
XX protection against the pathogenic strain when it had been allowed to
XX colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
XX consecutive inoculation), whereas no protection was provided when both
XX strains were inoculated simultaneously. The method of the invention may
XX be used to protect a wide variety of plants from pathogenic fungal
XX infection. Plants that may be protected include vegetables, crops such as
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CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC method is reliable and provides economical biocontrol of diseases caused
CC by Rhizoctonia solani. Sequences AA292459-292490 represent the ITS-5.8s
CC regions of ribosomal RNA-encoding DNA from a variety of Rhizoctonia
CC strains.
XX
XX Sequence 406 BP; 111 A; 85 C; 89 G; 121 T; 0 other;
XX
XX Query Match 67.8%; Score 166.2; DB 21; Length 406;
XX Best Local Similarity 88.5%; Pred. No. 5,2e-45;
XX Matches 215; Conservative 0; Mismatches 23; Indels 5; Gaps 3;
XX
Oy 5 AGGGGAATATAAAGTCGTACAGGTTTCGTAGTGTAACCTGCGGAGATCATTTATG 64
|||
Db 12 AGAGGAAGTAAAGTCGTACAGGTTTCGTAGTGTAACCTGCGGAGATCATTTATG 71
Oy 65 AATGATTTAGAGTTGGTTGCGTGGCTCCT--CCGGAGACATGTGACCTTTCTTT 122
|||
Db 72 AATGAACTAGAGTTGGTTGCGTGGCTCCTTCACTGGGCAATGTGACGCTTCTTT 131
|||
Oy 123 TCATCCACACACACCTGCGACTGTGAGACGGAGACCGTAAAAAAGTCTCCGTAT 182
|||
Db 132 TCATCCACACACACCTGCGACTGTGAGACGGAGAG--GCTTTAATTAAGTCTCCGTATC 190
Oy 183 TAAACCCACAAACCCCATGTTATTTAATGATGTAATGATGTAACGATCATTTAA 242
|||
Db 191 TTAATCACACAAAGTC--ATTTAATTAATTAATGATGTAATGATGTAACGATCATTTAGA 248
Oy 243 ACT 245
|||
Db 249 ACT 251

RESULT 12
AA292465
ID AA292465 standard; DNA: 411 BP.
AC AA292465;
XX
XX
XX 05-JUN-2000 (first entry)
XX
XX Rhizoctonia sp. isolate AGBO ribosomal DNA, ITS1-5.8s region.
XX
XX Antifungal; biocontrol; binucleate; non-pathogenic fungus;
XX strain identification; classification; internal transcribed spacer;
XX ITS region; 5.8s region; ribosomal; ds.
XX
XX Rhizoctonia sp.
XX
XX WO200004779-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-GB02406.
XX
XX 24-JUL-1998; 98GB-0016265.
XX
XX (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.
XX (RUFEL) RUFEL G K.
XX
XX Rubio Susan V, Salazar Torres O, Julian Esquivias M;
XX Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
XX Lopez Corcoles H;
XX
XX WPI: 2000-182492/16.
XX
XX Protection of plants including tomato, pepper, lettuce, radish,
XX parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
XX binucleate Rhizoctonia strain for biocontrol -
XX
XX Disclosure: Fig 1; 121pp; English.
XX
XX The invention relates to a novel method of protecting plants from
```





ID	AA292466	standard; DNA; 411 BP.
XX		
AC	AA292466;	
XX		
DT	05-JUN-2000	(first entry)
XX		
DE	Rhizoctonia sp. isolate AGBB ribosomal DNA, ITS1-5.8s region.	
XX		
KW	Antifungal; biocontrol; binucleate; non-pathogenic fungus;	
XX	strain identification; classification; internal transcribed spacer;	
KW	ITS region; 5.8s region; ribosomal; ds.	
XX		
OS	Rhizoctonia sp.	
XX		
PN	WO200004779-A1.	
XX		
PD	03-FEB-2000.	
XX		
PF	23-JUL-1999; 99WO-GB02406.	
XX		
PR	24-JUL-1998; 98GB-0016265.	
XX		
PA	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.	
XX	(RUFFE/) RUFFLES G K.	
PI	Rubio Susan V, Salazar Torres O, Julian Esquivias M;	
XX	Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;	
PI	Lopez Corcoles H;	
XX		
DR	WPI; 2000-182492/16.	
XX		
PT	Protection of plants including tomato, pepper, lettuce, radish,	
XX	parsley, sugar beet, rape, and onions against pathogenic fungi, uses a	
PT	binucleate Rhizoctonia strain for biocontrol -	
XX		
PS	Disclosure; Fig 1; 121pp; English.	
XX		
CC	The invention relates to a novel method of protecting plants from	
XX	pathogenic fungi. The method comprises biocontrol of pathogenic fungi	
CC	via the use of a non-pathogenic, binucleate Rhizoctonia strain. The	
XX	binucleate Rhizoctonia is selected by molecular detection of certain	
CC	internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences	
XX	(AA292445-AA292458), which vary between strains of these fungi. The	
CC	invention also encompasses a concentrate for use in plant protection	
XX	containing viable material from the binucleate Rhizoctonia strains of the	
CC	invention, and primers (AA292437-292444) for identifying these strains.	
XX	The strains of the invention are used as biocontrol agents for related	
CC	pathogenic fungi. Binucleate Rhizoctonia isolate Rab-F2 was tested for	
XX	its ability to protect tomato seedlings from the pathogenic Rhizoctonia	
CC	strain Me8.2. The Rhizoctonia strains were inoculated either	
XX	simultaneously or consecutively (the binucleate strain followed by the	
CC	pathogenic strain), and the protection effect indicated by the degree of	
XX	infected vegetal surface. The binucleate strain was found to provide	
CC	protection against the pathogenic strain when it had been allowed to	
XX	colonise the vegetal surface prior to pathogenic fungal infection (i.e.,	
CC	consecutive inoculation), whereas no protection was provided when both	
XX	strains were inoculated simultaneously. The method of the invention may	
CC	be used to protect a wide variety of plants from pathogenic fungal	
XX	infection. Plants that may be protected include vegetables, crops such as	
CC	oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The	
XX	method is reliable and provides economical biocontrol of diseases caused	
CC	by Rhizoctonia solani. Sequences AA292445-292490 represent the ITS-5.8s	
XX	regions of ribosomal RNA-encoding DNA from a variety of Rhizoctonia	
CC	strains.	
XX		
SO	Sequence 411 BP; 112 A; 90 C; 89 G; 120 T; 0 other;	
XX		
Query Match	57.5%;	Score 140.8; DB 21; Length 411;
Best Local Similarity	79.6%;	Pred. No. 1.4e-36;
Matches 191; Conservative	0;	Mismatches 47; Indels 2; Gaps 2
5	AGGGAATTAAGACGCTAACACAGCTTCCGTAGCGAACACCTCCGGAAGATCATATTG	64
11		

Db	15	AGGGAAGTAAAGTCGTAAAGAGTTTCCGTAGTGAACCTGGGAGAGATCATTTTG	74
Qy	65	AATGAATATAGAGTTGGTTGCTGCGGCT-CTCCGGAGCATGTGACGCTTTCTT	122
Db	75	AATGAAGTTAAGAGTCGTGGCTGGCTGCTCTTTGGAGCATGTGACGCTTTCTT	134
Qy	123	TCATCCACACACACCTGTGCACTGTGTGACGAGGAGACCCGTAAGAGTCCTCCCTAT	182
Db	135	TCATCCACACACACCTGTGCACTGTGTGACGAGGAGACCCGTAAGAGTCCTCCCTAT	194
Qy	183	TAAACACACAAACCCCATTTGTATTTAAATGAATGTAAATGTATTAACCATCATTTAA	242
Db	195	AAATCATATATCAAAACGATTTTAATGTAGACGATGTAACTTGATGTAAACCATCATTTAA	254
RESULT 15			
AAZ92464	ID	AAZ92464 standard; DNA; 410 BP.	
XX	AC	AAZ92464;	
XX	DT	05-JUN-2000 (first entry)	
XX	DE	Rhizoctonia sp. isolate AGP ribosomal DNA, ITS1-5.8s region.	
XX	KN	Antifungal; biocontrol; binucleate; non-pathogenic fungus;	
XX	KW	strain identification; classification; Internal transcribed spacer;	
XX	KW	ITS region; 5.8s region; ribosomal; ds.	
XX	OS	Rhizoctonia sp.	
XX	PN	WO200004779-A1.	
XX	PD	03-FEB-2000.	
XX	PE	23-JUL-1999; 99WO-GB02406.	
XX	PR	24-JUL-1998; 98GB-0016265.	
XX	PA	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.	
XX	PI	(RUFE/) RUFELES G K.	
XX	PI	Rubio Susan V, Salazar Torres O, Julian Esquivias M;	
XX	PI	Gonzalez Garcia V, Gomez-Acedo Gullon E, Munoz Gomez R;	
XX	PI	Lopez Corcoles H;	
XX	DR	WPI: 2000-182492/16.	
XX	PT	Protection of plants including tomato, pepper, lettuce, radish,	
XX	PT	parsley, sugar beet, rape, and onions against pathogenic fungi, uses a	
XX	PT	binucleate Rhizoctonia strain for biocontrol -	
XX	PS	Disclosure: Fig 1; 121pp; English.	
XX	CC	The invention relates to a novel method of protecting plants from	
XX	CC	pathogenic fungi. The method comprises biocontrol of pathogenic fungi	
XX	CC	via the use of a non-pathogenic, binucleate Rhizoctonia strain. The	
XX	CC	binucleate Rhizoctonia is selected by molecular detection of certain	
XX	CC	internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences	
XX	CC	(AAZ92445- AAZ92458), which vary between strains of these fungi. The	
XX	CC	invention also encompasses a concentrate for use in plant protection	
XX	CC	containing viable material from the binucleate Rhizoctonia strains of the	
XX	CC	invention, and primers (AAZ92437-292444) for identifying these strains.	
XX	CC	The strains of the invention are used as biocontrol agents for related	
XX	CC	pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for	
XX	CC	its ability to protect tomato seedlings from the pathogenic Rhizoctonia	
XX	CC	strain Me6.2. The Rhizoctonia strains were inoculated either	
XX	CC	simultaneously or consecutively (the binucleate stain followed by the	
XX	CC	pathogenic strain), and the protection effect indicated by the degree of	
XX	CC	infected vegetal surface. The binucleate strain was found to provide	
XX	CC	protection against the pathogenic strain when it had been allowed to	
XX	CC	colonise the vegetal surface prior to pathogenic fungal infection (i.e.,	
XX	CC	consecutive inoculation), whereas no protection was provided when both	

CC strains were inoculated simultaneously. The method of the invention may  
 CC be used to protect a wide variety of plants from pathogenic fungal  
 CC infection. Plants that may be protected include vegetables, crops such as  
 CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The  
 CC method is reliable and provides economical biocontrol of diseases caused  
 CC by Rhizoctonia solani. Sequences AN292459-292490 represent the ITS-5.8s  
 CC regions of ribosomal RNA-encoding DNA from a variety of Rhizoctonia  
 CC strains.

XX Sequence 410 BP; 112 A; 87 C; 91 G; 120 T; 0 other;

Query Match 54.5%; Score 133.6; DB 21; Length 410;  
 Best Local Similarity 80.2%; Pred. No. 3.4e-34;  
 Matches 194; Conservative 0; Mismatches 44; Indels 4; Gaps 3;

QY 5 AGGGGATATAAAGTCGTAAACAAGTTCCGTAGTGAACCTCGGAGAGATCATTTATG 64  
 Db 12 AGAGGAAGTAAAGTCGTAAACAAGTTCCGTAGTGAACCTCGGAGAGATCATTTATG 71  
 QY 65 AATGATA--TAGAGTTGTTGCTGCTGCT--CCTCCGGAGCATGTGCACGCTTCTCT 121  
 Db 72 AATGAACACTTGGAGTCGCTTGTGCTGCTGCTTTGGCAGCATGTGCACGCTTCTCT 131  
 QY 122 -TTTATCCACACACACCTGTGCTGTGAGAGGAGACCGTAAAAAGTCTTCCGCTCT 180  
 Db 132 ATTATTCACACACACCTGTGCTGTGAGAGGAGACCGTAAAAAGTCTTCCGCTCTG 191  
 QY 181 ATTAAACACACACACCTGTGCTGTGAGAGGAGACCGTAAAAAGTCTTCCGCTCT 240  
 Db 192 CTAAATTCAATATCAACACATTTAATGACTGAATGTACTGATGTAAACGATCATTTA 251  
 QY 241 AA 242  
 Db 252 AA 253

Search completed: March 2, 2003, 08:04:54  
 Job time : 132 secs



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OM nucleic - nucleic search, using SW model

Run on: March 2, 2003, 08:02:53 ; Search time 52 Seconds  
(without alignments)  
1444.919 Million cell updates/sec

Title: US-09-744-502-20

Perfect score: 245  
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Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_MA:\*

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2: /cgn2\_6/pdata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/pdata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/pdata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/pdata/1/lna/PCRTUS.COMB.seq:\*  
6: /cgn2\_6/pdata/1/lna/Backfilest1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.4	21.4	870	2	US-08-778-912A-4
2	52.4	21.4	870	4	US-09-541-941B-4
3	52.4	21.4	874	2	US-08-778-912A-1
4	52.4	21.4	874	4	US-09-541-941B-2
5	52.4	21.4	875	2	US-08-778-912A-2
6	52.4	21.4	875	2	US-08-778-912A-3
7	52.4	21.4	875	2	US-08-778-912A-5
8	52.4	21.4	875	2	US-08-778-912A-7
9	52.4	21.4	875	4	US-09-541-941B-1
10	52.4	21.4	875	4	US-09-541-941B-3
11	52.4	21.4	875	4	US-09-541-941B-5
12	52.4	21.4	875	4	US-09-541-941B-7
13	52.4	21.4	876	2	US-08-778-912A-6
14	52.4	21.4	876	4	US-09-541-941B-6
15	52.2	21.3	1788	2	US-08-867-820A-1
16	52.2	21.2	568	3	US-08-986-727-5
17	50.4	20.6	344	4	US-09-488-295-1
18	48.2	19.7	772	4	US-08-998-416-492
19	47.2	19.3	581	1	US-08-652-127C-6
20	47.2	19.3	583	1	US-08-652-127C-8
21	47.2	19.3	594	1	US-08-652-127C-5
22	47.2	19.3	594	4	US-08-645-073-1
23	46	18.8	617	3	US-08-986-727-2
24	46	18.8	1750	3	US-08-949-770-1
25	45.6	18.6	605	3	US-08-986-727-1
26	44.6	18.2	608	3	US-08-986-727-3
27	44.6	18.2	611	3	US-08-986-727-4

28	43	17.6	899	1	US-08-416-831B-1	Sequence 1, Appli
29	40.6	16.6	370	4	US-09-450-656-2	Sequence 2, Appli
30	40.4	16.5	917	4	US-09-541-941B-18	Sequence 18, Appli
31	40.4	16.5	918	4	US-09-541-941B-16	Sequence 16, Appli
32	40.4	16.5	918	4	US-09-541-941B-17	Sequence 17, Appli
33	40.4	16.5	918	4	US-09-541-941B-27	Sequence 27, Appli
34	40.2	16.4	312	1	US-08-400-580A-2	Sequence 2, Appli
35	39.2	16.0	267	1	US-08-400-580A-1	Sequence 1, Appli
36	39.2	16.0	267	1	US-08-400-580A-3	Sequence 3, Appli
37	38.8	15.8	898	4	US-09-541-941B-22	Sequence 22, Appli
38	38.8	15.8	898	4	US-09-541-941B-23	Sequence 23, Appli
39	38.8	15.8	898	4	US-09-541-941B-24	Sequence 24, Appli
40	38.8	15.8	898	4	US-09-541-941B-25	Sequence 25, Appli
41	38.8	15.8	918	4	US-09-541-941B-19	Sequence 19, Appli
42	37.2	15.2	815	4	US-09-541-941B-20	Sequence 20, Appli
43	37.2	15.2	904	4	US-09-541-941B-21	Sequence 21, Appli
44	35.2	14.4	4256	1	US-08-505-509-31	Sequence 31, Appli
45	35.2	14.4	4256	2	US-08-491-690A-31	Sequence 31, Appli

## ALIGNMENTS

RESULT 1  
US-08-778-912A-4/c  
; Sequence 4, Application US/08778912A  
; Patent No. 5876977  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Ngan, F N  
; APPLICANT: But, P P  
; APPLICANT: Shaw, P C  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT  
; TITLE OF INVENTION: TRADITIONAL POLYMORPHISM TEST FOR THE AUTHENTICATION OF  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,912A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chan, Albert Wai-Kit  
; REGISTRATION NUMBER: 36,479  
; REFERENCE/DOCKET NUMBER: 52188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 278 0400  
; TELEFAX: 212 391 0526  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 870 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-778-912A-4  
; Query Match 21.4%; Score 52.4; DB 2; Length 870;  
; Best local similarity 90.3%; Pred. No. 1.1e-08;  
; Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
; Oy 5 AGGGGAATMAAAGTCGTACAGCTTCCGTAGGTGAGTACCGGAGCATCATTTATTG 64

Db 762 AGAGGAAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGAGATCATTTGCG 703

QY 65 AA 66

Db 702 AA 701

## RESULT 2

US-09-541-941B-4/C  
; Sequence 4, Application US/09541941B  
; Patent No. 6309840  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Shaw, Pang Chui  
; APPLICANT: Paul, Pul-Hay  
; APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH  
; FILE REFERENCE: 2913/52188-2A  
; CURRENT APPLICATION NUMBER: US/09/541,941B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 870  
; TYPE: DNA  
; ORGANISM: P. Ginseng  
US-09-541-941B-4

Query Match 21.4%; Score 52.4; DB 4; Length 870;  
Best Local Similarity 90.3%; Pred. No. 1.1e-08;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGAATATAAAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGAGATCATTTATG 64

Db 762 AGAGGAAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGAGATCATTTGCG 703

QY 65 AA 66

Db 702 AA 701

## RESULT 3

US-08-778-912A-1/C  
; Sequence 1, Application US/08778912A  
; Patent No. 5876977  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Ngan, F N  
; APPLICANT: But, P P  
; APPLICANT: Shaw, P C  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT  
; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,912A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

NAME: Chan, Albert Wai-Kit  
REGISTRATION NUMBER: 36,479  
REFERENCE/DOCKET NUMBER: 52188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 278 0400  
TELEFAX: 212 391 0526

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 874 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-778-912A-1

Query Match 21.4%; Score 52.4; DB 2; Length 874;  
Best Local Similarity 90.3%; Pred. No. 1.1e-08;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGAATATAAAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGAGATCATTTATG 64

Db 760 AGAGGAAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGAGATCATTTGCG 701

QY 65 AA 66

Db 700 AA 699

## RESULT 4

US-09-541-941B-2/C  
; Sequence 2, Application US/09541941B  
; Patent No. 6309840  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Shaw, Pang Chui  
; APPLICANT: Paul, Pul-Hay  
; APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO  
; FILE REFERENCE: 2913/52188-2A  
; CURRENT APPLICATION NUMBER: US/09/541,941B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 874  
; TYPE: DNA  
; ORGANISM: P. Ginseng  
US-09-541-941B-2

Query Match 21.4%; Score 52.4; DB 4; Length 874;  
Best Local Similarity 90.3%; Pred. No. 1.1e-08;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGAATATAAAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGAGATCATTTATG 64

Db 760 AGAGGAAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGAGATCATTTGCG 701

QY 65 AA 66

Db 700 AA 699

## RESULT 5

US-08-778-912A-2/C  
; Sequence 2, Application US/08778912A  
; Patent No. 5876977  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Ngan, F N  
; APPLICANT: But, P P  
; APPLICANT: Shaw, P C  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT

;; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF  
;; TITLE OF INVENTION: TRADITIONAL CHINESE MEDICINES  
;; NUMBER OF SEQUENCES: 15  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Cooper & Dunham LLP  
;; STREET: 1185 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10036  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/778,912A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Chan, Albert Wai-Kit  
;; REGISTRATION NUMBER: 36,479  
;; REFERENCE/DOCKET NUMBER: 52188  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212 278 0400  
;; TELEFAX: 212 391 0526  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 875 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; US-08-778-912A-2

Query Match 21.4%; Score 52.4; DB 2; Length 875;  
Best Local Similarity 90.3%; Pred. No. 1.1e-08;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGATTAAGGTCGTAAACAGGTTCCGTAGTGGAACCTCGGAGGATCATATTG 64  
DB 761 AGAGGAAGAGAGAGTGTCTAACAAGGTTCCGTAGTGGAACCTCGGAGGATCATATTGCG 702

QY 65 AA 66  
DB 701 AA 700

RESULT 6  
US-08-778-912A-3/c  
; Sequence 3, Application US/08778912A  
; Patent No. 5876977  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Ngan, F N  
; APPLICANT: But, P P  
; APPLICANT: Shaw, P C  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT  
; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF  
; TITLE OF INVENTION: TRADITIONAL CHINESE MEDICINES  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/778,912A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Chan, Albert Wai-Kit  
;; REGISTRATION NUMBER: 36,479  
;; REFERENCE/DOCKET NUMBER: 52188  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212 278 0400  
;; TELEFAX: 212 391 0526  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 875 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; US-08-778-912A-3

Query Match 21.4%; Score 52.4; DB 2; Length 875;  
Best Local Similarity 90.3%; Pred. No. 1.1e-08;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGATTAAGGTCGTAAACAGGTTCCGTAGTGGAACCTCGGAGGATCATATTG 64  
DB 761 AGAGGAAGAGAGTGTCTAACAAGGTTCCGTAGTGGAACCTCGGAGGATCATATTGCG 702

QY 65 AA 66  
DB 701 AA 700

RESULT 7  
US-08-778-912A-5/c  
; Sequence 5, Application US/08778912A  
; Patent No. 5876977  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Ngan, F N  
; APPLICANT: But, P P  
; APPLICANT: Shaw, P C  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT  
; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF  
; TITLE OF INVENTION: TRADITIONAL CHINESE MEDICINES  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,912A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chan, Albert Wai-Kit  
; REGISTRATION NUMBER: 36,479  
; REFERENCE/DOCKET NUMBER: 52188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 278 0400  
; TELEFAX: 212 391 0526  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 875 base pairs  
; TYPE: nucleic acid





RESULT 11  
US-09-541-941B-5/c  
; Sequence 5, Application US/09541941B  
; Patent No. 6309840  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Shaw, Pang Chui  
; APPLICANT: Ngan, But/Hay  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPHISM  
; FILE REFERENCE: 2913/52188-ZA  
; CURRENT APPLICATION NUMBER: US/09/541,941B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 875  
; TYPE: DNA  
; ORGANISM: P. Japonicus  
US-09-541-941B-5

Query Match  
Best Local Similarity 90.3%; Pred. No. 1.1e-08;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTATTG 64  
DB 761 AGAGGAAGAGAGAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTGCG 702  
QY 65 AA 66  
DB 701 AA 700

RESULT 12  
US-09-541-941B-7/c  
; Sequence 7, Application US/09541941B  
; Patent No. 6309840  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Shaw, Pang Chui  
; APPLICANT: Ngan, But/Hay  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPHISM  
; FILE REFERENCE: 2913/52188-ZA  
; CURRENT APPLICATION NUMBER: US/09/541,941B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 875  
; TYPE: DNA  
; ORGANISM: P. Trifolium  
US-09-541-941B-7

Query Match  
Best Local Similarity 90.3%; Pred. No. 1.1e-08;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTATTG 64  
DB 762 AGAGGAAGAGAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTGTCG 703  
QY 65 AA 66  
DB 702 AA 701

RESULT 13  
US-08-778-912A-6/c  
; Sequence 6, Application US/08778912A

; Patent No. 5876977  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Ngan, F N  
; APPLICANT: But, P P  
; APPLICANT: Shaw, P C  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF TRADITIONAL CHINESE MEDICINES  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,912A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chan, Albert Wai-Kit  
; REGISTRATION NUMBER: 36,479  
; REFERENCE/DOCKET NUMBER: 52188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 278 0400  
; TELEFAX: 212 391 0526  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 876 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-778-912A-6

Query Match  
Best Local Similarity 21.4%; Score 52.4; DB 2; Length 876;  
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTATTG 64  
DB 762 AGAGGAAGAGAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTGCG 703  
QY 65 AA 66  
DB 702 AA 701

RESULT 14  
US-09-541-941B-6/c  
; Sequence 6, Application US/09541941B  
; Patent No. 6309840  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Jun  
; APPLICANT: Shaw, Pang Chui  
; APPLICANT: Ngan, But/Hay  
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPHISM  
; FILE REFERENCE: 2913/52188-ZA  
; CURRENT APPLICATION NUMBER: US/09/541,941B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 876



GenCore version 5.1.4-p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 08:04:59 ; Search time 69 seconds  
(without alignments)  
2214.299 Million cell updates/sec

Title: US-09-744-502-20

Perfect score: 245

Sequence: 1 ttagaaggggaataaaagtc.....tgaacgacatcataaact 245

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 460893 seqs, 31809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA.\*  
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2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
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10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
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13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	23.3	253	9	US-09-768-020-59
2	56.2	22.9	42999	9	US-09-799-462A-17
3	56.2	22.9	42999	9	US-10-125-767-17
4	56.2	22.9	42999	9	US-09-836-911A-17
5	52.4	21.4	870	10	US-09-897-231-4
6	52.4	21.4	874	10	US-09-897-231-2
7	52.4	21.4	875	10	US-09-897-231-1
8	52.4	21.4	875	10	US-09-897-231-3
9	52.4	21.4	875	10	US-09-897-231-5
10	52.4	21.4	875	10	US-09-897-231-7
11	52.4	21.3	1969	10	US-09-897-231-6
12	52.2	21.3	22118	9	US-09-880-107-2231
13	52.2	21.3	22118	9	US-09-799-462A-16
14	52.2	21.3	22118	9	US-10-125-767-16
15	52.2	21.3	22118	9	US-09-815-981-5
16	52.2	21.3	22118	9	US-09-836-911A-16
17	51.4	21.0	4240	9	US-09-938-842A-2248
18	48	19.6	1808	10	US-09-771-935B-17
19	40.4	16.5	917	10	US-09-897-231-18

20	40.4	16.5	918	10	US-09-897-231-16	Sequence 16, Appl
21	40.4	16.5	918	10	US-09-897-231-17	Sequence 17, Appl
22	40.4	16.5	1193	10	US-09-897-231-27	Sequence 27, Appl
23	40.4	16.5	640681	10	US-09-790-988-1	Sequence 1, Appl1
24	38.8	15.8	898	10	US-09-897-231-22	Sequence 22, Appl
25	38.8	15.8	898	10	US-09-897-231-23	Sequence 24, Appl
26	38.8	15.8	898	10	US-09-897-231-24	Sequence 25, Appl
27	38.8	15.8	898	10	US-09-897-231-25	Sequence 19, Appl
28	38.8	15.8	898	10	US-09-897-231-19	Sequence 20, Appl
29	37.2	15.2	815	10	US-09-897-231-20	Sequence 21, Appl
30	37.2	15.2	904	10	US-09-897-231-21	Sequence 1, Appl1
31	37.2	15.2	32998	9	US-10-027-806-1	Sequence 1, Appl1
32	37.2	15.2	32998	9	US-10-034-623-1	Sequence 2, Appl1
33	37.2	15.2	42432	9	US-10-027-806-2	Sequence 137, App
34	37.2	15.2	42432	9	US-10-034-623-2	Sequence 4, Appl1
35	36.2	14.8	140	10	US-09-925-299-137	Sequence 79, Appl
36	35.4	14.4	641	9	US-09-766-173C-4	Sequence 78, Appl
37	35	14.3	446	9	US-10-074-246-79	Sequence 77, Appl
38	35	14.3	600	9	US-10-074-246-78	Sequence 80, Appl
39	35	14.3	653	9	US-10-074-246-77	Sequence 3, Appl1
40	35	14.3	660	9	US-10-074-246-80	Sequence 7, Appl1
41	35	14.3	1467	10	US-09-726-774-3	Sequence 2, Appl1
42	35	14.3	1541	10	US-09-027-439-7	Sequence 5, Appl1
43	35	14.3	1541	10	US-09-726-774-2	Sequence 89, Appl
44	35	14.3	1544	10	US-09-726-774-5	
45	35	14.3	1549	10	US-09-912-020-89	

## ALIGNMENTS

RESULT 1  
US-09-768-020-59  
; Sequence 59, Application US/09768020  
; Patent No. US2002017447A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenspan, Ralph J.  
; APPLICANT: Edelman, Gerald M.  
; TITLE OF INVENTION: Method For Functional Mapping of An  
; TITLE OF INVENTION: Alzheimer's Disease Gene Network and For Identifying  
; FILE REFERENCE: P-NI 4577  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR FILING DATE: 2000-01-24  
; PRIOR APPLICATION NUMBER: US 09/490,243  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 253  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-768-020-59

Query Match 23.3%, Score 57; DB 9; Length 253;  
Best Local Similarity 92.3%; Pred. No. 4.3e-09;  
Matches 60; Conservative 0; Mismatches 5; Indels 0;

QY 5 AGGGAATTAATAAGTCGTACCAAGGTTTCCTAGTCACTGCGGGAAGATCTATTG 64  
DB 137 AGAGCAAGTAATAAGTCGTACCAAGGTTTCCTAGTCACTGCGGGAAGATCTATTG 196

QY 65 AATGA 69  
DB 197 TATTA 201

RESULT 2  
US-09-799-462A-17  
; Sequence 17, Application US/09799462A  
; Patent No. US20020160970A1  
; GENERAL INFORMATION:  
; APPLICANT: Hadlaczky, Gyula

```

Zalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,462A
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-4026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-799-462A-17

Query Match      22.9%   Score 56.2   DB 9;   Length 42999;
Best Local Similarity 63.9%;   Fred. No. 6.7e-08;
Matches 85; Conservative 0; Mismatches 48; Indels 0; Gaps 0

5 AGGGAATATAAGTCGTAAACAGCTTCCGTAGTGTAACCTGGCGAAGCATTTATTG 64
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5471 AAGGAGAAGTAAAAGTCGTACAAGGTTCCGTAGTGTAACCTGGCGAAGCATTTAAG 5530

QY 65 AATGAATATAGAGTTGGTTGCTGCCTGCGCTCTCCGGAACATGTGCACGCTTTCTTTTC 124
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Db 5531 GAGCCCGGAGGCGGAGGCCCGGGGGCGCCGCCGCCGCCGCGCTTCCCTCCGACAC 5590

QY 125 ATCGACACACACC 137
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5591 CCACCCCCCAC 5603

RESULT 3
US-10-125-767-17
Sequence 17, Application US/10125767
Patent No. US20020160410AI
GENERAL INFORMATION:

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1 APPLICANT: Hadlaczky, Gyula
2 TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
3 METHODS
4 FOR PREPARING ARTIFICIAL CHROMOSOMES
5
6 NUMBER OF SEQUENCES: 34
7
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Heller Ehrman White & McCauliffe LLP
10 STREET: 4350 La Jolla Village Drive, 7th Floor
11 CITY: San Diego
12 STATE: CA
13 COUNTRY: USA
14 ZIP: 92122
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette
18 COMPUTER: IBM Compatible
19 OPERATING SYSTEM: DOS
20 SOFTWARE: FastSeq Version 1.5
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/10/125,767
24 FILING DATE: 17-Apr-2002
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 09/724,693
28 FILING DATE: 28-NOV-2000
29 APPLICATION NUMBER: 08/835,682
30 FILING DATE: 10-APR-1997
31 APPLICATION NUMBER: 08/695,191
32 FILING DATE: 07-AUG-1996
33 APPLICATION NUMBER: 08/682,080
34 FILING DATE: 15-JUL-1996
35 APPLICATION NUMBER: 08/629,822
36 FILING DATE: 10-APR-1996
37
38 ATTORNEY/AGENT INFORMATION:
39 NAME: Seidman, Stephanie L
40 REGISTRATION NUMBER: 33,779
41 REFERENCE/DOCKET NUMBER: 24601-4020
42
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: 858-450-8403
45 TELEFAX: 858-587-5360
46
47 TELEX: <Unknown>
48
49 INFORMATION FOR SEQ ID NO: 17:
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51 SEQUENCE CHARACTERISTICS:
52 LENGTH: 42999 base pairs
53 TYPE: nucleic acid
54 STRANDEDNESS: single
55 TOPOLOGY: linear
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57 MOLECULE TYPE: Genomic DNA
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59 HYPOTHETICAL: NO
60 ANTI-SENSE: NO
61 FRAGMENT TYPE: <Unknown>
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64 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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69 Query Match 22.9%; Score 56.2; DB 9; Length 42999;
70 Best Local Similarity 63.9%; Pred. No. 6.7e-08;
71 Matches 85; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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Publication No. US20030033617A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4350 La Jolla Village Drive, 6th Floor
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,911A
FILING DATE: 17-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-Apr-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-Aug-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-Jul-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-4021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-836-911A-17

Query Match 22.9%; Score 56.2; DB 9; Length 42999;
Best Local Similarity 63.9%; Pred. No. 6.7e-08;
Matches . 85; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 5 AGGGGAATAAAAGTCGTAACAAGTTTCCTAGTGAACCTCGGAGAGATCATTTATTG 64
  || |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5471 AGAGGAAGTAAAGTCGTAAACAAGTTTCCTAGTGAACCTCGGAGAGATCATTTAAAG 5530

QY 65 AATGATATATAGATTGCTTGCCTGCTCTCCGGAGACGATGTGACGCTTTCTCTTC 124
  || |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5531 GACGCCGGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCCTCCGACAC 5590

QY 125 ATCCACACACAC 137
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Db 5591 CCACCCCCCACC 5603

RESULT 5
US-09-897-231-4/c
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Sequence 4, Application US/09897231
Patent No. US20020146705A1
GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 870
TYPE: DNA
ORGANISM: P. Ginseng
US-09-897-231-4

Query Match 21.4%; Score 52.4; DB 10; Length 870;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 65 AA 66
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Db 702 AA 701

RESULT 6
US-09-897-231-2/c
Sequence 2, Application US/09897231
Patent No. US20020146705A1
GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 874
TYPE: DNA
ORGANISM: P. Ginseng
US-09-897-231-2

Query Match 21.4%; Score 52.4; DB 10; Length 874;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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  || |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 760 AGAGGAAGGAGAGTCGTAAACAAGTTTCCTAGTGAACCTCGGAGAGATCATTTGCG 701

QY 65 AA 66
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Db 700 AA 699

RESULT 7
US-09-897-231-1/c
Sequence 1, Application US/09897231
Patent No. US20020146705A1
GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
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GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 07:55:23 ; Search time 1743 Seconds

(without alignments)  
2276.474 Million cell updates/sec

Title: US-09-744-502-20

Perfect score: 245  
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Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
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23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67.8	27.7	761	14	BU0383322
2	57.2	23.3	393	17	CI8A10
3	57.2	23.3	421	17	CI19H6
4	57.2	23.3	514	14	BP013583
5	57.2	23.3	544	10	AV953658
6	57.2	23.3	574	10	AV956116

7	57.2	23.3	598	17	CI2A11	AJ227080	Ciona	int	
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9	57.2	23.3	602	17	CI7G3	AJ227462	Ciona	int	
10	57.2	23.3	625	17	CI9G3	AJ227603	Ciona	int	
11	57.2	23.3	631	17	CI8E6	AJ227516	Ciona	int	
12	57.2	23.3	633	17	CI14B8	AJ226384	Ciona	int	
13	57.2	23.3	637	17	CI19C9	AJ226713	Ciona	int	
14	57.2	23.3	647	17	CI18E7	AJ226664	Ciona	int	
15	57.2	23.3	659	10	AV884174	AV884174	AV884174	Ciona	int
16	57.2	23.3	673	14	BP017870	BP017870	BP017870	Ciona	int
17	57.2	23.3	678	17	CI8B11	AJ227484	Ciona	int	
18	57.2	23.3	682	12	BE635943	BE635943	BE635943	Ciona	int
19	57.2	23.3	695	9	AA141495	AA141495	AA141495	Ciona	int
20	57.2	23.3	662	9	AA141460	AA141460	AA141460	Ciona	int
21	57.2	23.3	875	17	CNS06YCH	AL420855	T3	end of	
22	57.2	23.3	882	17	CNS06XIS	AL419786	T7	end of	
23	57.2	23.3	968	17	CNS06XLP	AL419891	T3	end of	
24	57.2	23.3	1001	17	CNS06XW7	AL420269	T3	end of	
25	57.2	23.3	1002	17	CNS06YDX	AL421303	T3	end of	
26	57.2	23.3	1021	17	CNS06YLOX	AL420360	T7	end of	
27	57.2	23.3	1021	17	CNS06XYQ	AL420377	T3	end of	
28	57.2	23.3	1024	17	CNS06XWF	AL420277	T3	end of	
29	57.2	23.3	1026	17	CNS06YOG	AL421286	T3	end of	
30	56.8	23.2	339	17	CI19B10	AJ226699	Ciona	int	
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33	56.4	23.0	316	17	AZ818673	AZ818673	2M0088A19		
34	56.4	23.0	341	17	AZ700886	RPCT-23-2			
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36	56.4	23.0	350	17	AZ003429	RPCT-23-3			
37	56.4	23.0	356	17	AZ284060	RPCT-23-4			
38	56.4	23.0	500	13	BM195843	BM195843	C0317609		
39	56.4	23.0	543	12	BS076758	H3005E06			
40	56.4	23.0	559	17	AZ806266	2M0068N09			
41	56.4	23.0	587	13	BM198750	C0406C05			
42	56.4	23.0	593	17	AZ361589	1M0106B06			
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#### ALIGNMENTS

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LOCUS BU0383322  
DEFINITION LIT0000228 Root-induced cDNA library from Laccaria bicolor Laccaria  
ACCESSION BU0383322  
VERSION BU0383322.1 GI:22473842  
KEYWORDS EST.  
SOURCE Laccaria bicolor.  
ORGANISM Laccaria bicolor.  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Tricholomataceae; Laccaria.

REFERENCE  
AUTHORS Podila, G.K., Brand, J.R. and Hynes, M.J.  
TITLE Root-induced cDNA library from Laccaria bicolor  
JOURNAL Unpublished (2002).  
COMMENT Contact: Dr. G.K. Podila  
Department of Biological Sciences  
University of Alabama  
Huntsville, AL 35899, USA  
Tel: 256 824 6263  
Fax: 256 824 6305  
Email: podilagemall.nah.edu.

FEATURES  
source

1. 761  
/organism="Laccaria bicolor"  
/db\_xref="taxon:29883"  
/clone\_lbp="Root-induced cDNA library from Laccaria bicolor"

/note="Laccaria bicolor in an interaction medium was exposed to Pinus resinosa roots for 6, 12, 24, 36, 48, 72 and 96 hours; the fungal tissue was then collected and frozen. Total mRNA was isolated from Laccaria tissue and pooled. This pooled mRNA was used to prepare a cDNA library. ESTs were randomly selected and sequenced to identify differentially expressed genes induced by root exudates using macroarray analysis."

BASE COUNT 168 a 167 c 192 g 225 t 9 others

Query Match 27.7%; Score 67.8; DB 14; Length 761;  
Best Local Similarity 73.1%; Pred. No. 1.6e-10;  
Matches 87; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 5 AGGGAATATAAAGTCGTACACAGTTCCGTAGTGACCTCGCGAAGATCATTTATTG 64  
DB 473 AGAGGAAGTAAAGTCGTACACAGTTCCGTAGTGACCTCGCGAAGATCATTTATTG 532  
QY 65 AATGAATATAGAGTTGCTGCTGCTCGCGAGCATGTGACAGCTTTCTCTTT 123  
DB 533 AATAAAGTATGCTGCTGCTGCTCGCGAGCATGTGCTGCTCATCATCTTT 591

RESULT 2  
CIBA10 393 bp DNA linear GSS 03-DEC-2000  
LOCUS Ciona intestinalis genomic fragment, clone BAI0, genomic survey  
DEFINITION  
SEQUENCE  
ACCESSION AJ227478.1 GI:2951302  
VERSION AJ227478.1  
KEYWORDS GSS: genome survey sequence.  
SOURCE Ciona intestinalis.  
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cloniidae; Clona.

REFERENCE 1 (bases 1 to 393)  
AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J., and Bird,A.  
TITLE Gene number in an invertebrate chordate, Ciona intestinalis  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)  
MEDLINE 98208558  
PUBMED 9539755

REFERENCE 2 (bases 1 to 393)  
AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,  
Clark,V.H., and Bird,A.  
TITLE Nonmethylated transposable elements and methylated genes in a  
JOURNAL chordate genome  
MEDLINE Science 283 (5405), 1164-1167 (1999)  
PUBMED 99148102  
PUBMED 10024242

REFERENCE 3 (bases 1 to 393)  
AUTHORS Simmen,M.W., and Bird,A.  
TITLE Sequence analysis of transposable elements in the sea squirt, Clona  
JOURNAL intestinalis  
MEDLINE Mol. Biol. Evol. 17 (11), 1685-1694 (2000)  
PUBMED 20523971

REFERENCE 4 (bases 1 to 393)  
AUTHORS Clark,V.H., Lettgeb,S., Charlton,J., Tweedie,S., Simmen,M.W., and  
Bird,A.P.  
TITLE Direct Submission  
JOURNAL Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's  
BUILDINGS, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:  
VCLARK@rsrv0.bio.ed.ac.uk  
COMMENT Vector: pBluescript KS.  
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QY 65 AATGAATATA 74  
DB 62 TATGAAGTA 71

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DEFINITION  
SEQUENCE  
ACCESSION AJ226748.1 GI:2950572  
VERSION AJ226748.1  
KEYWORDS GSS: genome survey sequence.  
SOURCE Ciona intestinalis.  
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cloniidae; Clona.

REFERENCE 1 (bases 1 to 421)  
AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J., and Bird,A.  
TITLE Gene number in an invertebrate chordate, Ciona intestinalis  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)  
MEDLINE 98208558  
PUBMED 9539755

REFERENCE 2 (bases 1 to 421)  
AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,  
Clark,V.H., and Bird,A.  
TITLE Nonmethylated transposable elements and methylated genes in a  
JOURNAL chordate genome  
MEDLINE Science 283 (5405), 1164-1167 (1999)  
PUBMED 99148102  
PUBMED 10024242

REFERENCE 3 (bases 1 to 421)  
AUTHORS Simmen,M.W., and Bird,A.  
TITLE Sequence analysis of transposable elements in the sea squirt, Clona  
JOURNAL intestinalis  
MEDLINE Mol. Biol. Evol. 17 (11), 1685-1694 (2000)  
PUBMED 20523971  
PUBMED 11070056

REFERENCE 4 (bases 1 to 421)  
AUTHORS Clark,V.H., Lettgeb,S., Charlton,J., Tweedie,S., Simmen,M.W., and  
Bird,A.P.  
TITLE Direct Submission  
JOURNAL Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's  
BUILDINGS, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:  
VCLARK@rsrv0.bio.ed.ac.uk  
COMMENT Vector: pBluescript KS.  
FEATURES Location/Qualifiers  
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/organism="Ciona intestinalis"  
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/dev\_stage="adult"

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QY 65 AATGAATATA 74

Db 282 TATGAAGCTA 291

# RESULT 4

BP013583/c

## LOCUS

BP013583 Nori Satoh unpublished cDNA library, young adult Ciona

BP013583

## ACCESSION

BP013583

## VERSION

BP013583.1

## KEYWORDS

EST

## SOURCE

ORGANISM

Ciona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 514)

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

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Location/Qualifiers

1. 514

/organism="Ciona intestinalis"

/db\_xref="taxon:7719"

/clone="ciad57113"

/clone\_lib="Nori Satoh unpublished cDNA library, young

adult"

/tissue\_type="whole animal"

/dev\_stage="young adult"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

124 a 141 c 129 g 120 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 14; Length 514;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 72 AGAGGAAGTAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 13

QY 65 AATGAATATA 74

DB 12 TAAGAAAGTA 3

RESULT 5

AV953658/c

LOCUS

AV953658 Nori Satoh unpublished cDNA library, young adult Ciona

AV953658

ACCESSION

AV953658

VERSION

AV953658.1

KEYWORDS

EST

SOURCE

ORGANISM

Ciona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 544)

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

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Location/Qualifiers

1. 544

/organism="Ciona intestinalis"

/db\_xref="taxon:7719"

/clone="ci1b43913"

/clone\_lib="Nori Satoh unpublished cDNA library, tailbud

embryo"

/tissue\_type="whole animal"

/dev\_stage="tailbud embryo"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

113 a 187 c 143 g 129 t 2 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 10; Length 574;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 494 AGAGGAAGTAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 435

Tel: 81-75-753-4081

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Location/Qualifiers

1. 544

/organism="Ciona intestinalis"

/db\_xref="taxon:7719"

/clone="ciad08a09"

/clone\_lib="Nori Satoh unpublished cDNA library, young

adult"

/tissue\_type="whole animal"

/dev\_stage="young adult"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

123 a 137 c 142 g 122 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 10; Length 544;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 159 AGAGGAAGTAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 100

QY 65 AATGAATATA 74

DB 99 TAAGAAAGTA 90

RESULT 6

AV996116/c

LOCUS

AV996116 Nori Satoh unpublished cDNA library, tailbud embryo Ciona

AV996116

ACCESSION

AV996116

VERSION

AV996116.1

KEYWORDS

EST

SOURCE

ORGANISM

Ciona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 574)

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

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Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. 574

/organism="Ciona intestinalis"

/db\_xref="taxon:7719"

/clone="ci1b43913"

/clone\_lib="Nori Satoh unpublished cDNA library, tailbud

embryo"

/tissue\_type="whole animal"

/dev\_stage="tailbud embryo"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

113 a 187 c 143 g 129 t 2 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 10; Length 574;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 494 AGAGGAAGTAAAGTCGTACAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 435

QY 65 AATGAATATA 74  
 DB 434 TAGAAGGTA 425

RESULT 7  
 C12A11 598 bp DNA linear GSS 03-DEC-2000  
 LOCUS Ciona intestinalis genomic fragment, clone 2A11, genomic survey  
 DEFINITION sequence.

ACCESSION AJ227080  
 VERSION AJ227080.1 GI:2950906  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Ciona intestinalis.  
 ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 598)  
 AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J., and Bird,A.  
 TITLE Gene number in an invertebrate chordate, Ciona intestinalis  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)  
 MEDLINE 98208558  
 PUBMED 9539755

REFERENCE 2 (bases 1 to 598)  
 AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R., Clark,V.H., and Bird,A.  
 TITLE Nonmethylated transposable elements and methylated genes in a chordate genome  
 JOURNAL Science 283 (5405), 1164-1167 (1999)  
 MEDLINE 99148102  
 PUBMED 10024242

REFERENCE 3 (bases 1 to 598)  
 AUTHORS Simmen,M.W., and Bird,A.  
 TITLE Sequence analysis of transposable elements in the sea squirt, Ciona intestinalis  
 JOURNAL Mol. Biol. Evol. 17 (11), 1685-1694 (2000)  
 MEDLINE 20523971  
 PUBMED 11070056

REFERENCE 4 (bases 1 to 598)  
 AUTHORS Clark,V.H., Lettgeb,S., Charlton,J., Tweedie,S., Simmen,M.W., and Bird,A.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact: VCLARK@serv0.dio.ed.ac.uk  
 COMMENT Location/Qualifiers  
 FEATURES source 1..598 /organism="Ciona intestinalis" /db\_xref="taxon:7719" /clone="2A11" /dev\_stage="adult"

BASE COUNT 135 a 150 c 178 g 134 t 1 others

ORIGIN

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 Best Local Similarity 88.6%; Pred. No. 3.4e-07;  
 Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGAATTAAGTCGTAAACAGGTTTCGTAGTGAACCTCGGAGAGATCATTTATG 64  
 DB 276 AGAGGAGTAAGTAAGTCGTAAACAGGTTTCGTAGTGAACCTCGGAGAGATCATTTAAG 335

QY 65 AATGAATATA 74  
 DB 336 TATGAAGGTA 345

RESULT 8  
 AV966409/c 602 bp mRNA linear EST 14-MAR-2002  
 LOCUS AV966409 Nori Satoh unpublished cDNA library, young adult Ciona  
 DEFINITION intestinalis cDNA clone ctad16113 5', mRNA sequence.

ACCESSION AV966409  
 VERSION AV966409.1 GI:19456105  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis.  
 ORGANISM Ciona intestinalis.  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 602)  
 AUTHORS Satoh,N., Satou,Y., Kohara,Y., and Shin-I,T.  
 TITLE Expressed genes in Ciona intestinalis  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Nori Satoh  
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 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
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 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
 source 1..602 /organism="Ciona intestinalis" /db\_xref="taxon:7719" /clone="ctad16113" /clone\_id="Nori Satoh unpublished cDNA library, young adult" /issue\_type="whole animal" /dev\_stage="young adult" /note="Vector: pBluescript SK"

BASE COUNT 139 a 166 c 158 g 138 t 1 others

ORIGIN

Query Match 23.3%; Score 57.2; DB 10; Length 602;  
 Best Local Similarity 88.6%; Pred. No. 3.4e-07;  
 Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGAATTAAGTCGTAAACAGGTTTCGTAGTGAACCTCGGAGAGATCATTTATG 64  
 DB 165 AGAGGAGTAAGTAAGTCGTAAACAGGTTTCGTAGTGAACCTCGGAGAGATCATTTAAG 106

QY 65 AATGAATATA 74  
 DB 105 TAGAAGGTA 96

RESULT 9  
 C17G3 602 bp DNA linear GSS 03-DEC-2000  
 LOCUS C17G3 Ciona intestinalis genomic fragment, clone 7G3, genomic survey  
 DEFINITION sequence.

ACCESSION AJ227462  
 VERSION AJ227462.1 GI:2951285  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Ciona intestinalis.  
 ORGANISM Ciona intestinalis.  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 602)  
 AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J., and Bird,A.  
 TITLE Gene number in an invertebrate chordate, Ciona intestinalis  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)  
 MEDLINE 98208558  
 PUBMED 9539755

REFERENCE 2 (bases 1 to 602)  
 AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R., Clark,V.H., and Bird,A.  
 TITLE Nonmethylated transposable elements and methylated genes in a chordate genome  
 JOURNAL Science 283 (5405), 1164-1167 (1999)  
 MEDLINE 99148102  
 PUBMED 10024242

REFERENCE 3 (bases 1 to 602)  
 AUTHORS Simmen,M.W., and Bird,A.  
 TITLE Sequence analysis of transposable elements in the sea squirt, Ciona





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VERSION      AJ226664.1 GI:2950124
KEYWORDS     GSS: genome survey sequence.
SOURCE       Ciona intestinalis.
ORGANISM     Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cloniidae; Clona.
REFERENCE    1 (bases 1 to 647)
AUTHORS      Simmen,M.W., Leltgeb,S., Clark,V.H., Jones,S.J. and Bird,A.
TITLE        Gene number in an invertebrate chordate, Ciona intestinalis
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
MEDLINE      98208558
PUBMED       9539755
REFERENCE    2 (bases 1 to 647)
AUTHORS      Simmen,M.W., Leltgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,
TITLE        Clark,V.H. and Bird,A.
JOURNAL      Nonmethylated transposable elements and methylated genes in a
MEDLINE      chordate genome
PUBMED       science 283 (5405), 1164-1167 (1999)
REFERENCE    3 (bases 1 to 647)
AUTHORS      Simmen,M.W. and Bird,A.
TITLE        Sequence analysis of transposable elements in the sea squirt, Ciona
JOURNAL      Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
MEDLINE      20523971
PUBMED       11070056
REFERENCE    4 (bases 1 to 647)
AUTHORS      Clark,V.H., Leltgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and
TITLE        Bird,A.P.
JOURNAL      Direct Submission
MEDLINE      Submitted (28-FEB-1998) ICM, University of Edinburgh, King's
PUBMED       Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
REFERENCE    Vector: pBluescript KS.
AUTHORS      Location/Qualifiers
TITLE        1. .647
JOURNAL      /organism="Ciona intestinalis"
MEDLINE      /db_xref="taxon:7719"
PUBMED       /clone="18E7"
REFERENCE    /dev_stage="adult"
AUTHORS      BASE COUNT      140 a      197 c      147 g      151 t      12 others
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Best Local Similarity 88.6%; Pred. No. 3.5e-07;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY      5 AGGGGAATATAAAGTCGTAAACAGGTTCCGTAGTGACCTGCGGAGATCATATTG 64
      || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      384 AGAGGAAGTAAAGTCGTAAACAGGTTCCGTAGTGACCTGCGGAGATCATATTG 64
QY      65 AATGAATATA 74
      || ||| ||
DB      324 TATGAAGTA 315

RESULT 15
AVB84174/c
LOCUS       AVB84174      659 bp      mRNA      linear      EST 08-NOV-2001
DEFINITION AVB84174 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
ACCESSION   AVB84174
VERSION     AVB84174.1 GI:16871698
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
ORGANISM   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cloniidae; Clona.
REFERENCE   1 (bases 1 to 659)
AUTHORS     Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE       Expressed genes in Ciona intestinalis
JOURNAL     Unpublished (2000)

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COMMENT      Contact: Nori Satoh
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              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES     Location/Qualifiers
              source
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              /organism="Ciona intestinalis"
              /db_xref="taxon:7719"
              /clone="rc1b4k17"
              /clone_lib="Nori Satoh unpublished cDNA library, tailbud
              embryo"
              /issue_type="whole animal"
              /dev_stage="tailbud embryo"
              /note="Vector: pBluescript SK"
BASE COUNT   147 a      194 c      167 g      150 t      1 others
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Best Local Similarity 88.6%; Pred. No. 3.5e-07;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY      5 AGGGGAATATAAAGTCGTAAACAGGTTCCGTAGTGACCTGCGGAGATCATATTG 64
      || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      205 AGAGGAAGTAAAGTCGTAAACAGGTTCCGTAGTGACCTGCGGAGATCATATTG 64
QY      65 AATGAATATA 74
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DB      145 TATGAAGTA 136

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Job time : 1750 secs

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